

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:34:01 ; Search time 21.8636 Seconds
(without alignments)
94.378 Million cell updates/sec

Title: US-09-931-700-2

Perfect score: 76

Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*

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21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
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23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	13	AAW25159	Human preproadreno
2	57	75.0	31	AAW25160	Human preproadreno
3	57	75.0	31	AAW25162	Adrenomedullin pep
4	57	75.0	31	AAE09827	Human adrenomedullin
5	57	75.0	40	AAW25168	Adrenomedullin pep
6	57	75.0	50	AAE09819	Rat adrenomedullin
7	57	75.0	52	AAW25110	Human adrenomedullin
8	57	75.0	52	AAW25179	Adrenomedullin pep
9	57	75.0	52	AAW25175	Adrenomedullin pep

10	57	75.0	52	22	AAE09818	Human adrenomedullin
11	57	75.0	52	24	ABP55104	Human adrenomedullin
12	57	75.0	53	22	AAW25111	Glycine extended h
13	57	75.0	53	22	AAW25112	Glycine extended a
14	57	75.0	53	24	ABJ18665	Universal stress p
15	57	75.0	62	22	AAW25113	Linker peptide-adr
16	57	75.0	120	22	AAW25122	UspA(1-57)-(A)-(GS
17	57	75.0	120	22	AAW25123	UspA(1-56)-(DD)-(G
18	57	75.0	120	24	ABJ18669	Universal stress p
19	57	75.0	120	24	ABJ18670	Universal stress p
20	57	75.0	147	22	AAW25124	UspA(1-84)-(A)-(GS
21	57	75.0	147	24	ABJ18671	Universal stress p
22	57	75.0	170	22	AAW25114	Thioredoxin-(GS)SG
23	57	75.0	185	22	AAW25115	Human adrenomedullin
24	57	75.0	185	22	AAW25116	Rat adrenomedullin
25	57	75.0	185	22	AAW25117	Human adrenomedullin
26	57	75.0	185	22	AAW25118	Rat adrenomedullin
27	57	75.0	185	24	ABP72347	Adrenomedullin, in
28	57	75.0	188	22	AAW25119	Porcine adrenomedu
29	57	75.0	188	22	AAW25120	Porcine adrenomedu
30	57	75.0	206	24	ABJ18668	Universal stress p
31	57	75.0	206	24	ABJ18669	Adrenomedullin pep
32	57	75.0	206	24	ABJ18670	Adrenomedullin pep
33	57	75.0	206	24	ABJ18671	Adrenomedullin pep
34	57	75.0	206	24	ABJ18672	Adrenomedullin pep
35	57	75.0	206	24	ABJ18673	Adrenomedullin pep
36	57	75.0	206	24	ABJ18674	Adrenomedullin pep
37	57	75.0	206	24	ABJ18675	Adrenomedullin pep
38	57	75.0	206	24	ABJ18676	Adrenomedullin pep
39	57	75.0	206	24	ABJ18677	Adrenomedullin pep
40	57	75.0	206	24	ABJ18678	Adrenomedullin pep
41	57	75.0	206	24	ABJ18679	Adrenomedullin pep
42	57	75.0	206	24	ABJ18680	Adrenomedullin pep
43	57	75.0	206	24	ABJ18681	Adrenomedullin pep
44	57	75.0	206	24	ABJ18682	Adrenomedullin pep
45	57	75.0	206	24	ABJ18683	Adrenomedullin pep

ALIGNMENTS

RESULT 1

AAW25159
ID AAW25159 standard; peptide; 13 AA.

XX AC AAW25159;

XX DT 08-DEC-1997 (first entry)

XX DE Human preproadrenomedullin derived immunogen, P071.

XX KW Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone;
XX KW skin; blood related; disease; type II diabetes; preclampsia;
XX KW neurotransmission regulation; allergy; mast cell degranulation;
XX KW antibacterial; antifungal; wound repair.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..13

XX FT /note= "residues 122-131 of preproadrenomedullin

XX FT with Tyr-Gly-Gly attached at N-terminus"

XX FT Modified-site 13 /note= "amidated"

XX FT

XX PN WO9707214-A1.

XX XX 27-FEB-1997.

XX PD

XX XX 16-AUG-1996;

XX PF 96WO-US13286.

XX XX 12-MAR-1996;

XX PR 96US-0013172.

XX PR 18-AUG-1995;

XX PR 95US-0002514.

PA	(CONJ-) CONJUCHEM INC.
XX	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI	WPI; 2001-112059/12.
PT	Modifying and attaching therapeutic peptides to albumin prevents
XX	peptidase degradation, useful for increasing length of in vivo activity
DR	-
XX	Disclosure; Page 499-500; 733pp; English.
PS	The present invention describes a modified therapeutic peptide (I)
XX	comprising a therapeutically active amino acid region (III) and a
CC	reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC	a less therapeutically active amino acid region (IV), which covalently
CC	bonds with amino/hydroxyl/thiol groups on blood components to form a
CC	peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC	factors and neurotransmitters, to protect them from peptidase activity
CC	in vivo for the treatment of various disorders. Endogenous therapeutic
CC	peptides are not suitable as drug candidates as they require frequent
CC	administration due to rapid degradation by peptidases in the body.
CC	Modifying and attaching therapeutic peptides to albumin prevents or
CC	reduces the action of peptidases to increase length of activity (half
CC	life) and specificity as bonding to large molecules decreases
CC	intracellular uptake and interference with physiological processes.
CC	AAB90829 to AAB92441 represent peptides which can be used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 31 AA;
	Query Match 75.0%; Score 57; DB 22; Length 31;
	Best Local Similarity 100.0%; Pred. No. 0.006;
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	4 HQIQFTDKD 13
Db	7 HQIQFTDKD 16
RESULT 4	
AAE09827	AAE09827 standard; peptide; 31 AA.
ID	AAE09827
AC	AAE09827
XX	
XX	29-NOV-2001 (first entry)
DT	
XX	Human adrenomedullin peptide #2.
DE	
XX	Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW	CGRP-receptor identification; adrenomedullin.
KX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 31
FT	/note= "C-terminal amide"
XX	
PN	US6268474-B1.
XX	
PD	31-JUL-2001.
XX	
PX	30-APR-1998; 98US-0070504.
XX	
PR	30-APR-1998; 98US-0070504.
XX	(UYCR-) UNIV CREIGHTON.
PA	
XX	Smith DD, Saha S, Abel PW;
PI	WPI; 2001-564216/63.
DR	

XX	Vasoactive peptides useful for inhibiting calcitonin gene related
PT	peptide receptor activity -
XX	
PS	Claim 5; Column 6; 24pp; English.
XX	
CC	The invention relates to antagonists of the vasoactive peptide
CC	calcitonin gene related peptide (CGRP) and other members of the
CC	CGRP superfamily. The invention also relates to amino the terminal
CC	modifications of peptides to improve their ability to bind to a
CC	member of the CGRP-receptor super-family. CGRP antagonists are
CC	used for inhibiting CGRP activity which can be used in vitro e.g.
CC	in assays to identify and/or isolate CGRP receptors or with intact
CC	cells either in vitro or in vivo to inhibit the effect of CGRP
CC	binding to its receptor. The present sequence is human
CC	adrenomedullin peptide.
XX	
SQ	Sequence 31 AA;
	Query Match 75.0%; Score 57; DB 22; Length 31;
	Best Local Similarity 100.0%; Pred. No. 0.006;
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	4 HQIQFTDKD 13
Db	7 HQIQFTDKD 16
RESULT 5	
AAB91768	AAB91768 standard; Peptide; 40 AA.
ID	AAB91768
XX	
AC	AAB91768;
XX	
DT	22-JUN-2001 (first entry)
XX	
DE	Adrenomedullin peptide (AM) SEQ ID NO:944.
XX	
KW	Protection; endogenous therapeutic peptide; peptidase; conjugation;
KX	blood component; modification; succinimidyl; maleimido group; amino;
KW	hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200069900-A2.
XX	
PD	23-NOV-2000.
XX	
PF	17-MAY-2000; 2000WO-US13576.
XX	
PR	17-MAY-1999; 99US-0134406.
PR	10-SEP-1999; 99US-0153406.
PR	15-OCT-1999; 99US-0159783.
XX	
XX	(CONJ-) CONJUCHEM INC.
PA	
PI	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI	WPI; 2001-112059/12.
DR	
XX	Modifying and attaching therapeutic peptides to albumin prevents
PT	peptidase degradation, useful for increasing length of in vivo activity
PT	-
XX	Disclosure; Page 502; 733pp; English.
XX	
CC	The present invention describes a modified therapeutic peptide (I)
CC	comprising a therapeutically active amino acid region (III) and a
CC	reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC	a less therapeutically active amino acid region (IV), which covalently
CC	bonds with amino/hydroxyl/thiol groups on blood components to form a
CC	peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC	factors and neurotransmitters, to protect them from peptidase activity
CC	in vivo for the treatment of various disorders. Endogenous therapeutic
CC	peptides are not suitable as drug candidates as they require frequent
CC	administration due to rapid degradation by peptidases in the body.
CC	Modifying and attaching therapeutic peptides to albumin prevents or
CC	reduces the action of peptidases to increase length of activity (half
CC	life) and specificity as bonding to large molecules decreases
CC	intracellular uptake and interference with physiological processes.
CC	AAB90829 to AAB92441 represent peptides which can be used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 31 AA;

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX SQ Sequence 40 AA;

Query Match 75.0%; Score 57; DB 22; Length 40;
 Best Local Similarity 100.0%; Pred. No. 0.008;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 16 HQIYQFTDKD 25

RESULT 6

AAE09819
 ID AAE09819 standard; peptide; 50 AA.

XX AC AAE09819;

XX XX 29-NOV-2001 (first entry)

XX XX Rat adrenomedullin peptide.

XX XX Rat; vasoactive peptide; calcitonin gene related peptide; CGRP;
 KW CGRP-receptor identification; adrenomedullin.

XX OS Rattus sp.

XX XX US6268474-B1.

XX XX 31-JUL-2001.

XX PF 30-APR-1998; 98US-0070504.

XX PR 30-APR-1998; 98US-0070504.

XX XX (UYCR-) UNIV CREIGHTON.

XX PI Smith DD, Saha S, Abel PW;

XX XX WPI; 2001-564216/63.

XX PT Vasoactive peptides useful for inhibiting calcitonin gene related
 PT peptide receptor activity -

XX PS Claim 5; Column 25-26; 24pp; English.

XX CC The invention relates to antagonists of the vasoactive peptide
 CC calcitonin gene related peptide (CGRP) and other members of the
 CC CGRP superfamily. The invention also relates to amino the terminal
 CC modifications of peptides to improve their ability to bind to a
 CC member of the CGRP-receptor super-family. CGRP antagonists are
 CC used for inhibiting CGRP activity which can be used in vitro e.g.
 CC in assays to identify and/or isolate CGRP receptors or with intact
 CC cells either in vitro or in vivo to inhibit the effect of CGRP
 CC binding to its receptor. The present sequence is rat adrenomedullin
 CC peptide.

XX SQ Sequence 50 AA;

Query Match 75.0%; Score 57; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 26 HQIYQFTDKD 35

RESULT 7

AAB75110
 ID AAB75110 standard; Protein; 52 AA.

XX AC AAB75110;

XX XX 31-JUL-2001 (first entry)

XX XX Human adrenomedullin (AM) protein.

XX KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
 KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.

XX OS Homo sapiens.

XX XX WO200127310-A1.

XX XX 19-APR-2001.

XX XX 10-OCT-2000; 2000WO-JP07023.

XX XX 15-OCT-1999; 99JP-0294147.

XX XX (SHIO) SHIONOGI & CO LTD.

XX XX Takimoto A, Mitsuda Y, Nakayama T, Mitsuhashi K;

XX XX WPI; 2001-282044/29.

XX XX N-PSDB; AAB19806.

XX PT Producing adrenomedullin useful for pharmaceutical and diagnostic
 PT application comprises producing fused adrenomedullin precursor using a
 PT recombinant host -

XX PS Disclosure; Page 45; 75pp; Japanese.

XX CC The present invention describes a method (M1) for producing
 CC adrenomedullin precursor. The method comprises: (a) producing the fused
 CC protein using a recombinant host cell; (b) restricted digestion of the
 CC fused protein by a protease followed by collection of sediment; and
 CC (c) dissolving the sediment and extracting adrenomedullin precursor.
 CC The method can be used for the production of adrenomedullin precursor
 CC for pharmaceutical and diagnostic applications. AAB19806 to AAB19866
 CC and AAB75110 to AAB75124 represent sequences which are used in the
 CC exemplification of the present invention.

XX SQ Sequence 52 AA;

Query Match 75.0%; Score 57; DB 22; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 28 HQIYQFTDKD 37

RESULT 8

AAB91759
 ID AAB91759 standard; Peptide; 52 AA.

XX AC AAB91759;

XX XX 22-JUN-2001 (first entry)

XX XX Adrenomedullin peptide (AM) SEQ ID NO:935.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

PN WO200069900-A2.
 XX

PD 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT

PS Disclosure; Page 498; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

SQ Sequence 52 AA;

Query Match 75.0%; Score 57; DB 22; Length 52;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13

|||||

Db 28 HQIYQFTDKD 37

RESULT 9

AAB91765

ID AAB91765 standard; Peptide; 52 AA.

XX AAB91765;

XX 22-JUN-2001 (first entry)

XX Adrenomedullin peptide (AM) SEQ ID NO:941.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT

PS Disclosure; Page 501; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

SQ Sequence 52 AA;

Query Match 75.0%; Score 57; DB 22; Length 52;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13

|||||

Db 27 HQIYQFTDKD 36

RESULT 10

AAE09818

ID AAE09818 standard; peptide; 52 AA.

XX AAE09818;

XX 29-NOV-2001 (first entry)

XX Human adrenomedullin peptide #1.

XX Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
 KW CGRP-receptor identification; adrenomedullin.
 XX Homo sapiens.

XX US6268474-B1.

XX 31-JUL-2001.

XX 30-APR-1998; 98US-0070504.

XX 30-APR-1998; 98US-0070504.
 XX (UYCR-) UNIV CREIGHTON.
 XX Smith DD, Saha S, Abel PW;
 XX WPI; 2001-564216/63.
 XX Vasoactive peptides useful for inhibiting calcitonin gene related
 PT peptide receptor activity -
 XX Claim 5; Column 25-26; 24pp; English.
 XX The invention relates to antagonists of the vasoactive peptide
 CC calcitonin gene related peptide (CGRP) and other members of the
 CC CGRP superfamily. The invention also relates to amino the terminal
 CC modifications of peptides to improve their ability to bind to a
 CC member of the CGRP-receptor super-family. CGRP antagonists are
 CC used for inhibiting CGRP activity which can be used in vitro e.g.
 CC in assays to identify and/or isolate CGRP receptors or with intact
 CC cells either in vitro or in vivo to inhibit the effect of CGRP
 CC binding to its receptor. The present sequence is human
 CC adrenomedullin peptide.
 XX Sequence 52 AA;
 SQ

Query Match 75.0%; Score 57; DB 22; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 DB 28 HQIYQFTDKD 37
 |||||

RESULT 11
 ABP55104
 ID ABP55104 standard; Peptide; 52 AA.
 XX AC ABP55104;
 XX 07-FEB-2003 (first entry)
 XX Human adrenomedullin.
 XX Adrenomedullin; human; protein engineering; solubility;
 KW aggregation; hypotensive; vasodilator; cyclic.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 16..21
 XX WO200283734-A2.
 XX 24-OCT-2002.
 XX 17-APR-2002; 2002WO-GB01778.
 XX 17-APR-2001; 2001GB-0009438.
 XX (ISIS-) ISIS INNOVATION LTD.
 XX Zurdo J, Dobson CM;
 XX WPI; 2003-046916/04.
 XX New modified human calcitonin peptide having reduced aggregation,
 PT useful for the treatment of Paget's disease, hypercalcemia and/or
 PT osteoporosis -
 XX Example; Page 21; 35pp; English.
 PS

XX The present sequence is that of human adrenomedullin, a potent
 CC hypotensive and vasodilator. The invention provides modified
 CC calcitonin and related peptides, such as adrenomedullin, that
 CC have at least 70% identity to the native form but are modified
 CC such that the tendency of the peptide to aggregate is reduced.
 CC Preferred regions for modification include those for which the
 CC peptide is polymorphic amongst different species, which increase
 CC the propensity of the peptide to form local interactions of the
 CC alpha-helical type, or which reduce the number of hydrophobic
 CC residues or increase the net charge of the peptide. When
 CC aggregation is reduced or prevented, lower doses of the drug can
 CC be used. Side-effects and undesired responses are minimised by
 CC retaining high sequence identity to the human peptide.
 XX Sequence 52 AA;
 SQ

Query Match 75.0%; Score 57; DB 24; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 DB 28 HQIYQFTDKD 37
 |||||

RESULT 12
 AAB75111
 ID AAB75111 standard; Protein; 53 AA.
 XX AC AAB75111;
 XX 31-JUL-2001 (first entry)
 XX Glycine extended human adrenomedullin (AM-gly) protein.
 XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
 KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 XX Homo sapiens.
 XX WO200127310-A1.
 XX 19-APR-2001.
 XX 10-OCT-2000; 2000WO-JP07023.
 XX 15-OCT-1999; 99JP-0294147.
 XX (SHIO) SHIONOGI & CO LTD.
 XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
 XX WPI; 2001-282044/29.
 XX N-PSDB; AAH19807.
 XX Producing adrenomedullin useful for pharmaceutical and diagnostic
 PT application comprises producing fused adrenomedullin precursor using a
 PT recombinant host -
 XX Example 1; Page 46; 75pp; Japanese.
 XX The present invention describes a method (M1) for producing
 CC adrenomedullin precursor. The method comprises: (a) producing the fused
 CC protein using a recombinant host cell; (b) restricted digestion of the
 CC fused protein by a protease followed by collection of sediment; and
 CC (c) dissolving the sediment and extracting adrenomedullin precursor.
 CC The method can be used for the production of adrenomedullin precursor
 CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
 CC and AAB75110 to AAB75124 represent sequences which are used in the
 CC exemplification of the present invention.
 XX Sequence 53 AA;
 SQ

Query Match 75.0%; Score 57; DB 22; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 28 HQIYQFTDKD 37

RESULT 13
 AAB75112
 ID AAB75112 standard; Protein; 53 AA.
 XX
 AC AAB75112;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Glycine extended adrenomedullin (AM-gly) protein.
 XX
 KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
 KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200127310-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 10-OCT-2000; 2000WO-JP07023.
 XX
 PR 15-OCT-1999; 99JP-0294147.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 PI Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
 XX
 DR WPI; 2001-282044/29.
 DR N-PSDB; AAH19808.
 XX
 PT Producing adrenomedullin useful for pharmaceutical and diagnostic
 PT application comprises producing fused adrenomedullin precursor using a
 PT recombinant host -
 XX
 PS Disclosure; Page 47; 75pp; Japanese.
 XX
 CC The present invention describes a method (M1) for producing
 CC adrenomedullin precursor. The method comprises: (a) producing the fused
 CC protein using a recombinant host cell; (b) restricted digestion of the
 CC fused protein by a protease followed by collection of sediment; and
 CC (c) dissolving the sediment and extracting adrenomedullin precursor.
 CC The method can be used for the production of adrenomedullin precursor
 CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
 CC and AAB75110 to AAB75124 represent sequences which are used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 53 AA;

Query Match 75.0%; Score 57; DB 22; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 28 HQIYQFTDKD 37

RESULT 14
 ABJ18665
 ID ABJ18665 standard; Protein; 53 AA.
 XX
 AC ABJ18665;

XX 27-FEB-2003 (first entry)
 DT
 XX Universal stress protein A (uspA)-related protein #1.
 DE
 XX
 KW Fusion peptide; universal stress peptide; UspA; linker peptide;
 KW large scale peptide production.
 XX
 OS Unidentified.
 XX
 PN WO200283907-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 04-APR-2002; 2002WO-JP03374.
 XX
 PR 10-APR-2001; 2001JP-0111088.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 PI Mitsuda Y;
 PI
 DR WPI; 2003-067381/06.
 DR N-PSDB; ABT14525.
 XX
 PT Fusion polypeptide of Escherichia coli universal stress peptide with a
 PT target peptide, useful for efficient large scale production of the
 PT target peptide comprising expression of the fusion polypeptide followed
 PT by cleavage -
 XX
 PS Claim 4; Page 30; 49pp; Japanese.
 XX
 CC The invention comprises a novel fusion peptide which contains an
 CC Escherichia coli universal stress protein (USP), a linker peptide and a
 CC target peptide. The fusion protein is cleavable by a protease. The fusion
 CC peptide of the invention is useful for the efficient large scale
 CC production of peptides. The present amino acid sequence represents a
 CC protein that was used in the invention.
 XX
 SQ Sequence 53 AA;

Query Match 75.0%; Score 57; DB 24; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 28 HQIYQFTDKD 37

RESULT 15
 AAB75113
 ID AAB75113 standard; Protein; 62 AA.
 XX
 AC AAB75113;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Linker peptide-adrenomedullin (AM) precursor protein.
 XX
 KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
 KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200127310-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 10-OCT-2000; 2000WO-JP07023.
 XX
 PR 15-OCT-1999; 99JP-0294147.

XX (SHIO) SHIONOGI & CO LTD.
 XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
 XX WPI: 2001-282044/29.
 DR N-PSDB; AAH19809.
 XX Producing adrenomedullin useful for pharmaceutical and diagnostic
 PT application comprises producing fused adrenomedullin precursor using a
 PT recombinant host -
 XX Claim 20; Page 48; 75pp; Japanese.
 PS
 XX The present invention describes a method (M1) for producing
 CC adrenomedullin precursor. The method comprises: (a) producing the fused
 CC protein using a recombinant host cell; (b) restricted digestion of the
 CC fused protein by a protease followed by collection of sediment; and
 CC (c) dissolving the sediment and extracting adrenomedullin precursor.
 CC The method can be used for the production of adrenomedullin precursor
 CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
 CC and AAB75110 to AAB75124 represent sequences which are used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 62 AA;

Query Match 75.0%; Score 57; DB 22; Length 62;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 HQIYQFTDKD 13
 DB 37 HQIYQFTDKD 46
 |||||

Search completed: October 14, 2003, 08:38:46
 Job time : 22.8636 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:37:31 ; Search time 8.56818 Seconds
(without alignments)
64.196 Million cell updates/sec

Title: US-09-931-700-2

Perfect score: 76

Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	76	100.0	13	4	US-09-011-922A-2
2	57	75.0	13	4	US-09-280-501-15
3	57	75.0	26	4	US-09-280-501-1
4	57	75.0	27	4	US-09-280-501-2
5	57	75.0	28	4	US-09-280-501-3
6	57	75.0	29	4	US-09-280-501-4
7	57	75.0	30	4	US-09-280-501-5
8	57	75.0	31	3	US-09-070-504-23
9	57	75.0	31	4	US-09-011-922A-3
10	57	75.0	31	4	US-09-011-922A-14
11	57	75.0	31	4	US-09-280-501-9
12	57	75.0	38	4	US-09-280-501-6
13	57	75.0	40	4	US-09-280-501-8
14	57	75.0	40	4	US-09-280-501-11
15	57	75.0	50	3	US-09-070-504-15
16	57	75.0	50	4	US-09-280-501-7
17	57	75.0	52	3	US-09-070-504-14
18	57	75.0	185	1	US-08-233-389C-1
19	57	75.0	185	2	US-08-801-863-1
20	57	75.0	185	2	US-08-486-596A-1
21	57	75.0	185	2	US-09-004-713-1
22	57	75.0	188	1	US-08-233-389C-3
23	57	75.0	188	2	US-08-801-863-3
24	57	75.0	188	2	US-08-486-596A-3
25	57	75.0	188	2	US-09-004-713-3
26	44	57.9	23	4	US-09-280-501-17
27	44	57.9	514	4	US-09-266-965-116

28	41	53.9	264	4	US-09-252-991A-19737	Sequence 19737, A
29	41	53.9	317	4	US-09-634-238-241	Sequence 241, App
30	40	52.6	157	4	US-09-252-991A-25900	Sequence 25900, A
31	39	51.3	433	4	US-09-252-991A-21838	Sequence 21838, A
32	39	51.3	686	3	US-09-368-169-8	Sequence 8, Appli
33	38.5	50.7	374	3	US-09-306-881-2	Sequence 2, Appli
34	38.5	50.7	396	4	US-09-107-532A-5962	Sequence 5962, Ap
35	38	50.0	418	4	US-09-107-532A-6073	Sequence 6073, Ap
36	37	48.7	302	4	US-09-599-360B-75	Sequence 75, Appl
37	37	48.7	1844	4	US-08-851-567B-53	Sequence 53, Appl
38	37	48.7	2504	4	US-08-851-567B-12	Sequence 12, Appl
39	36	47.4	196	3	US-07-998-289B-4	Sequence 4, Appli
40	36	47.4	231	4	US-09-107-532A-3675	Sequence 3675, Ap
41	36	47.4	291	4	US-09-252-991A-24398	Sequence 24398, A
42	36	47.4	347	3	US-09-333-423-2	Sequence 2, Appli
43	36	47.4	470	4	US-09-266-965-118	Sequence 118, App
44	36	47.4	484	4	US-09-581-831-2	Sequence 2, Appli
45	36	47.4	514	4	US-09-134-001C-4347	Sequence 4347, Ap

ALIGNMENTS

RESULT 1

US-09-011-922A-2
; Sequence 2, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez, Edward
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-8849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: P071
; OTHER INFORMATION: YGG-PreproAM (122-131)
US-09-011-922A-2

Query Match 100.0%; Score 76; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 13
Db 1 YGGHQIYQFTDKD 13

RESULT 2
US-09-280-501-15
; Sequence 15, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-15

Query Match 75.0%; Score 57; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 1 HQIYQFTDKD 10

RESULT 3
US-09-280-501-1
; Sequence 1, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-1

Query Match 75.0%; Score 57; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 2 HQIYQFTDKD 11

RESULT 4
US-09-280-501-2
; Sequence 2, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-2

Query Match 75.0%; Score 57; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 3 HQIYQFTDKD 12

RESULT 5
US-09-280-501-3
; Sequence 3, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-3

Query Match 75.0%; Score 57; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 4 HQIYQFTDKD 13

RESULT 6
US-09-280-501-4
; Sequence 4, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-4

Query Match 75.0%; Score 57; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
|||||
Db 5 HQIYQFTDKD 14

RESULT 7
US-09-280-501-5
; Sequence 5, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-5

Query Match 75.0%; Score 57; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
|||||
Db 6 HQIYQFTDKD 15

RESULT 8
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.

; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/070,504
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-23

Query Match 75.0%; Score 57; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
|||||
Db 7 HQIYQFTDKD 16

RESULT 9
US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J. Hook; William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 3:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: P072
; OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3

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Query Match          75.0%; Score 57; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 HQIYQFTDKD 13
        |||||
Db      7 HQIYQFTDKD 16

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RESULT 10
US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; OTHER INFORMATION: Synthetic homolog of
; OTHER INFORMATION: two-thirds of the intact AM peptide
US-09-011-922A-14

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Query Match          75.0%; Score 57; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 HQIYQFTDKD 13
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Db      7 HQIYQFTDKD 16

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RESULT 11
US-09-280-501-9
; Sequence 9, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 31
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-280-501-9

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Query Match          75.0%; Score 57; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 HQIYQFTDKD 13
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Db      7 HQIYQFTDKD 16

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RESULT 12
US-09-280-501-6
; Sequence 6, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:

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; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-6

Query Match 75.0%; Score 57; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 14 HQIYQFTDKD 23

RESULT 13
US-09-280-501-8
; Sequence 8, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-8

Query Match 75.0%; Score 57; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 18 HQIYQFTDKD 27

RESULT 14
US-09-280-501-11
; Sequence 11, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562

; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-11

Query Match 75.0%; Score 57; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 16 HQIYQFTDKD 25

RESULT 15
US-09-070-504-15
; Sequence 15, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-15

Query Match 75.0%; Score 57; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 26 HQIYQFTDKD 35

Search completed: October 14, 2003, 08:41:21
Job time : 9.56818 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:40:27 ; Search time 26 Seconds
(without alignments)
80.564 Million cell updates/sec

Title: US-09-931-700-2

Perfect score: 76

Sequence: 1 YGGHQTQYQTDKD 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	13	9 US-09-931-700-2	Sequence 2, Appli
2	57	75.0	31	9 US-09-931-700-3	Sequence 3, Appli
3	57	75.0	31	9 US-09-931-700-14	Sequence 14, Appli
4	57	75.0	31	9 US-09-813-345-23	Sequence 23, Appli
5	57	75.0	50	9 US-09-813-345-15	Sequence 15, Appli
6	57	75.0	52	9 US-09-813-345-14	Sequence 14, Appli
7	57	75.0	52	15 US-10-197-954-2	Sequence 2, Appli
8	44	57.9	514	12 US-09-953-348-116	Sequence 116, App
9	44	57.9	514	15 US-10-267-255-116	Sequence 116, App
10	44	57.9	833	15 US-10-027-000-2	Sequence 2, Appli
11	41	53.9	519	8 US-08-781-986A-5230	Sequence 5230, Ap
12	39	51.3	1356	10 US-09-801-368-306	Sequence 306, App
13	38	50.0	325	10 US-09-738-626-5238	Sequence 5238, Ap
14	37	48.7	161	10 US-09-738-626-6765	Sequence 6765, Ap
15	37	48.7	302	11 US-09-895-298-66	Sequence 66, Appli

16	37	48.7	345	11	US-09-895-298-120	Sequence 120, App
17	37	48.7	688	12	US-10-254-074-2	Sequence 2, Appli
18	37	48.7	1844	15	US-10-242-056-53	Sequence 53, Appli
19	37	48.7	2504	9	US-09-817-514A-8	Sequence 8, Appli
20	37	48.7	2504	15	US-10-242-056-12	Sequence 12, Appli
21	36.5	48.0	451	12	US-10-355-430-32	Sequence 32, Appli
22	36	47.4	118	10	US-09-764-868-1062	Sequence 1062, Ap
23	36	47.4	118	11	US-09-955-999-71	Sequence 71, Appli
24	36	47.4	123	10	US-09-764-868-630	Sequence 630, App
25	36	47.4	143	10	US-09-764-868-1075	Sequence 1075, Ap
26	36	47.4	143	11	US-09-955-999-103	Sequence 103, App
27	36	47.4	213	9	US-09-815-242-4889	Sequence 4889, Ap
28	36	47.4	218	12	US-10-238-075-1104	Sequence 1104, Ap
29	36	47.4	231	9	US-09-815-242-10536	Sequence 10536, A
30	36	47.4	265	9	US-09-815-242-12332	Sequence 12332, A
31	36	47.4	265	9	US-09-815-242-12870	Sequence 12870, A
32	36	47.4	285	9	US-09-815-242-13144	Sequence 13144, A
33	36	47.4	433	12	US-10-137-870-6	Sequence 6, Appli
34	36	47.4	433	12	US-10-140-018-6	Sequence 6, Appli
35	36	47.4	433	12	US-10-140-021-6	Sequence 6, Appli
36	36	47.4	433	12	US-10-140-274-6	Sequence 6, Appli
37	36	47.4	433	12	US-10-140-471-6	Sequence 6, Appli
38	36	47.4	433	12	US-10-140-807-6	Sequence 6, Appli
39	36	47.4	433	12	US-10-140-922-6	Sequence 6, Appli
40	36	47.4	433	12	US-10-140-924-6	Sequence 6, Appli
41	36	47.4	433	12	US-10-140-926-6	Sequence 6, Appli
42	36	47.4	433	12	US-10-141-698-6	Sequence 6, Appli
43	36	47.4	433	12	US-10-141-702-6	Sequence 6, Appli
44	36	47.4	433	12	US-10-141-704-6	Sequence 6, Appli
45	36	47.4	433	12	US-10-142-421-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-931-700-2
; Sequence 2, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUWITITA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202US4
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide,
; OTHER INFORMATION: P071, YGG-PreproAM (amino acids 122-131)

US-09-931-700-2

Query Match 100.0%; Score 76; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 13
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Db 1 YGGHQIYQFTDKD 13

RESULT 2

US-09-931-700-3
; Sequence 3, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; FILE REFERENCE: 2026-4202US4
; CURRENT APPLICATION NUMBER: US/09/931,700
; PRIOR FILING DATE: 2001-08-16
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide, P072,
; OTHER INFORMATION: PreproAM (amino acids 116-146)
US-09-931-700-3

Query Match 75.0%; Score 57; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
|||||
Db 7 HQIYQFTDKD 16

RESULT 3

US-09-931-700-14
; Sequence 14, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES

; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; FILE REFERENCE: 2026-4202US4
; CURRENT APPLICATION NUMBER: US/09/931,700
; PRIOR FILING DATE: 2001-08-16
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide,
; OTHER INFORMATION: Synthetic homolog of AM (P072), Structural amino
; OTHER INFORMATION: acid sequence representing two-thirds of the
; OTHER INFORMATION: intact AM peptide
US-09-931-700-14

Query Match 75.0%; Score 57; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
|||||
Db 7 HQIYQFTDKD 16

RESULT 4

US-09-813-345-23
; Sequence 23, Application US/09813345
; Patent No. US20020068814A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; Saba, Shankar
; Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; OTHER INFORMATION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch & Gebhardt, P.A.
; STREET: 119 No. US20020068814A1th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/813,345
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-813-345-23

Query Match 75.0%; Score 57; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
|||||
Db 7 HQIYQFTDKD 16

RESULT 5

US-09-813-345-15

; Sequence 15, Application US/09813345

; Patent No. US20020068814A1

; GENERAL INFORMATION:

; APPLICANT: Smith, Derek D.
; Saha, Shankar
; Abel, Peter W.; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; SUPERFAMILY AND METHODS OF USE

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mueeting, Raasch & Gebhardt, P.A.
; STREET: 119 No. US20020068814A1 Fourth Street

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/813,345

; FILING DATE: 20-Mar-2001

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: McCormack, Myra H

; REGISTRATION NUMBER: 36,602

; REFERENCE/DOCKET NUMBER: 180.00020101

; TELEPHONE: 612/305-1228

; TELEFAX: 612/305-1228

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; TYPE: amino acids

; LENGTH: 50 amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-813-345-15

Query Match

75.0%; Score 57; DB 9; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
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Db 26 HQIYQFTDKD 35

RESULT 6

US-09-813-345-14

; Sequence 14, Application US/09813345

; Patent No. US20020068814A1

; GENERAL INFORMATION:

; APPLICANT: Smith, Derek D.

; Saha, Shankar

; Abel, Peter W.

; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR

; SUPERFAMILY AND METHODS OF USE

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mueeting, Raasch & Gebhardt, P.A.

; STREET: 119 No. US20020068814A1 Fourth Street

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/813,345

; FILING DATE: 20-Mar-2001

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: McCormack, Myra H

; REGISTRATION NUMBER: 36,602

; REFERENCE/DOCKET NUMBER: 180.00020101

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612/305-1228

; TELEFAX: 612/305-1228

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 52 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-813-345-14

Query Match

75.0%; Score 57; DB 9; Length 52;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
|||||
Db 28 HQIYQFTDKD 37

RESULT 7

US-10-197-954-2

; Sequence 2, Application US/10197954

; Publication No. US20030119021A1

; GENERAL INFORMATION:

; APPLICANT: K*ster, Hubert

; APPLICANT: Siddiqi, Subaib

; APPLICANT: Little, Daniel

; TITLE OF INVENTION: Capture Compounds, Collections Thereof

; AND Methods For Analyzing The Proteome And Complex

; TITLE OF INVENTION: Compositions

; FILE REFERENCE: 24743-2305

; CURRENT APPLICATION NUMBER: US/10/197,954

; CURRENT FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 60/306,019

; PRIOR FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: 60/314,123

; PRIOR FILING DATE: 2001-08-21

; PRIOR APPLICATION NUMBER: 60/363,433

; PRIOR FILING DATE: 2002-03-11

; NUMBER OF SEQ ID NOS: 149

; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-2

Query Match          75.0%; Score 57; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GHIYQFTDKD 13
    |||||
Db 28 HQIYQFTDKD 37

RESULT 8
US-09-953-348-116
; Sequence 116, Application US/09953348
; Publication No. US20030134398A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, David. H
; APPLICANT: Mao, Yingqiang
; APPLICANT: Varoglu, Mustafa
; APPLICANT: He, Min
; APPLICANT: Sheldon, Paul
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: 600.530US1
; CURRENT APPLICATION NUMBER: US/09/953,348
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: PCT/US00/06394
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/266965
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Streptomyces lavendulae
US-09-953-348-116

Query Match          57.9%; Score 44; DB 12; Length 514;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHQIYQFTD 11
    |||
Db 66 GGHGIYQFYD 75

RESULT 9
US-10-267-255-116
; Sequence 116, Application US/10267255
; Publication No. US20030124689A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/10/267,255
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 08/524,447
; PRIOR FILING DATE: 1996-08-19
; PRIOR APPLICATION NUMBER: PCT/US94/11279
; PRIOR FILING DATE: 1994-10-06
; PRIOR APPLICATION NUMBER: US 08/133,963
; PRIOR FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Streptomyces lavendulae
US-10-267-255-116

Query Match          57.9%; Score 44; DB 15; Length 514;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHQIYQFTD 11
    |||
Db 66 GGHGIYQFYD 75

RESULT 10
US-10-027-000-2
; Sequence 2, Application US/10027000
; Publication No. US20030119006A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Goedegebuur, Frits
; APPLICANT: Ward, Michael
; APPLICANT: Yao, Jian
; TITLE OF INVENTION: BGL4 Beta-Glucosidase and Nucleic Acids
; FILE REFERENCE: GC696
; CURRENT APPLICATION NUMBER: US/10/027,000
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-10-027-000-2

Query Match          57.9%; Score 44; DB 15; Length 833;
Best Local Similarity 53.8%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 13
    |||
Db 682 YVGRIYEFADKD 694

RESULT 11
US-08-781-986A-5230
; Sequence 5230, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5230:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5230

Query Match 53.9%; Score 41; DB 8; Length 519;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHIYQFTDKD 13
   |||||
Db 454 GGRIGQFSSKD 465

RESULT 12
US-09-801-368-306
; Sequence 306, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amr
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 306
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-306

Query Match 51.3%; Score 39; DB 10; Length 1356;
Best Local Similarity 62.5%; Pred. No. 4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOIYQFTD 11
   |:::|
Db 496 HEVIEFTD 503

RESULT 13
US-09-738-626-5238
; Sequence 5238, Application US/09738626
; Publication No. US20020197605A1

```

```

; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5238
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5238

Query Match 50.0%; Score 38; DB 10; Length 325;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHIYQFTDKD 13
   ||:::|
Db 13 GGPEVLEFTD 24

RESULT 14
US-09-738-626-6765
; Sequence 6765, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6765
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6765

Query Match 48.7%; Score 37; DB 10; Length 161;
Best Local Similarity 63.8%; Pred. No. 93;

```

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GHQIYQFTDKD 13
 ||:| |
 Db 62 CHRISNTTDDK 72

RESULT 15

US-09-895-298-66
 ; Sequence 66, Application US/09895298
 ; Publication No. US20030078405A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 47 Human Secreted Proteins
 ; FILE REFERENCE: P2035P1
 ; CURRENT APPLICATION NUMBER: US/09/895,298
 ; CURRENT FILING DATE: 2001-07-02
 ; PRIOR APPLICATION NUMBER: 09/591,16
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/29950
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: 60/113,006
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: 60/112,809
 ; PRIOR FILING DATE: 1998-12-17
 ; NUMBER OF SEQ ID NOS: 231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 66
 ; LENGTH: 302
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (237)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-895-298-66

Query Match 48.7%; Score 37; DB 11; Length 302;
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDK 12
 | | | | |
 Db 176 YPGIQQVYTFER 187

Search completed: October 14, 2003, 08:53:16
 Job time : 26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2003, 08:36:56 ; Search time 7.38636 Seconds
(without alignments)
169.257 Million cell updates/sec

Title: US-09-931-700-2
Perfect score: 76
Sequence: 1 YGGHQIYQFTBKD 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	75.0	185	2 JN0684	adrenomedullin pre
2	57	75.0	185	2 JN0766	adrenomedullin pre
3	57	75.0	188	2 S41600	adrenomedullin - p
4	51	67.1	643	2 S76069	hypothetical prote
5	45	59.2	776	2 T02702	hypothetical prote
6	44	57.9	2231	2 D71870	hypothetical prote
7	42	55.3	280	2 H70089	hypothetical prote
8	42	55.3	324	2 A87544	hypothetical prote
9	42	55.3	350	2 T21106	hypothetical prote
10	42	55.3	563	2 T09378	hypothetical prote
11	41	53.9	185	2 C86705	hypothetical prote
12	41	53.9	467	2 T21690	hypothetical prote
13	41	53.9	514	2 D89775	hypothetical prote
14	40	52.6	146	2 G83445	conserved hypothet
15	40	52.6	260	2 H71979	probable type II r
16	40	52.6	275	2 T32005	hypothetical prote
17	39.5	52.0	606	2 T40556	hypothetical prote
18	39	51.3	176	2 B35697	transcription fact
19	39	51.3	310	2 H69986	hypothetical prote
20	39	51.3	444	1 F69130	histidine-tRNA lig
21	39	51.3	705	2 JX0194	prolyl oligopeptid
22	39	51.3	1356	2 S51389	ROM2 protein - yea
23	38.5	50.7	322	2 T22410	hypothetical prote
24	38	50.0	165	2 F69819	conserved hypothet
25	38	50.0	254	2 H70860	probable enoyl-CoA
26	38	50.0	267	2 AH0859	periplasmic fibri
27	38	50.0	284	2 T23866	hypothetical prote
28	38	50.0	387	2 T28402	ORF MSV241 leucine
29	38	50.0	391	2 H89859	hypothetical prote

30	38	50.0	425	2 S17759	protein kinase, ca
31	38	50.0	532	2 T14335	protein kinase, ca
32	38	50.0	564	2 A96999	pectate lyase rela
33	38	50.0	571	2 S8356	pepr protein - Sta
34	38	50.0	586	2 A95167	ABC transporter, A
35	38	50.0	586	2 H98032	hypothetical prote
36	38	50.0	952	2 E84534	hypothetical prote
37	38	50.0	1337	2 T30291	dextranase - Strept
38	37.5	49.3	569	2 JS0101	alpha-amylase (EC
39	37	48.7	105	2 T28838	hypothetical prote
40	37	48.7	164	2 AG0539	probable lipoprote
41	37	48.7	227	2 H82344	rfrt protein VC025
42	37	48.7	250	2 B86817	oxidoreductase ypi
43	37	48.7	253	2 F90507	sugar phosphate pu
44	37	48.7	257	2 E82238	imidazoleglycerol-
45	37	48.7	285	2 T29832	hypothetical prote

ALIGNMENTS

RESULT 1
JN0684
adrenomedullin precursor - human
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C:Accession: JC2351; JN0684; PN0548; JN0476
R:Kitamura, K.; Sakata, J.; Kangawa, K.; Hino, J.; Matsuo, K.; Kitamura, K.; Eto,
R.; Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuo, K.; Kitamura, K.; Eto,
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A:Title: Genomic structure of human adrenomedullin gene.
A:Reference number: JC2351; MUID:94354869; PMID:8074714
A:Accession: JC2351
A:Molecule type: DNA
A:Residues: 1-185 <JSH>
A:Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
R:Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A:Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
A:Reference number: JN0684; MUID:93343928; PMID:7688224
A:Accession: JN0684
A:Molecule type: mRNA
A:Residues: 1-185 <KIT>
A:Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A:Accession: PN0548
A:Molecule type: protein
A:Residues: 22-41 <KL2>
R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A:Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A:Reference number: JN0476; MUID:93249425; PMID:8387282
A:Accession: JN0476
A:Molecule type: protein
A:Residues: 95-146 <KL3>
A:Experimental source: pheochromocytoma
C:Genetics:
A:Gene: GDB:ADM
A:Cross-references: GDB:217070; OMIM:103275
A:Map position: lppter-llqter
A:Introns: 33/2; 83/2
C:Keywords: amidated carboxyl end; blood pressure control; hormone
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-185/Product: proadrenomedullin #status predicted <PRU>
F:22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F:95-146/Product: adrenomedullin #status experimental <MAT>
F:147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F:110-115/Disulfide bonds: #status experimental
F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match 75.0%; Score 57; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: D71870

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2231 <ARN>

A:Cross-references: GB:AB001522; GB:AB001439; NID:94155505; PIDN:AA06506.1; PID:9415550

A:Experimental source: strain J99

C:Genetics:

A:Gene: jhp0928

Query Match 57.9%; Score 44; DB 2; Length 2231;

Best Local Similarity 53.8%; Pred. No. 40;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 13

Db 620 YGNHKIYSSNDKE 632

RESULT 7

H70089

hypothetical protein yycI - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: H70089

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertea

A.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Kroch, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Scoffone, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, K.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: H70089

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-280 <KUN>

A:Cross-references: GB:299124; GB:AL009126; NID:92636442; PIDN:CAB16075.1; PID:g2636585

A:Experimental source: strain 168

C:Genetics:

A:Gene: yycI

C:Superfamily: Bacillus subtilis hypothetical protein yycI

Query Match 55.3%; Score 42; DB 2; Length 280;

Best Local Similarity 72.7%; Pred. No. 9.7;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTD 11

Db 152 YEGHYIQFTD 162

RESULT 8

A87544

hypothetical protein CC2378 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: A87544

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

N, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: A87544

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-324 <STO>

A:Cross-references: GB:AE005673; NID:gl3423911; PIDN:AAK24349.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2378

C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homolo

Query Match 55.3%; Score 42; DB 2; Length 324;

Best Local Similarity 50.0%; Pred. No. 11;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13

Db 244 GGHEVYINIGDND 255

RESULT 9

T21106

hypothetical protein F19B6.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21106

R:Thomas, K.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z19375

A:Accession: T21106

A>Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-350 <WIL>

A:Cross-references: EMBL:Z69635; NID:gl200023; PIDN:CAA93458.1; GSPDB:GN00022; CESP:F

A:Experimental source: clone F19B6

C:Genetics:

A:Gene: CESP:F19B6.3

A:Map position: 4

A:Introns: 180/3; 274/2

Query Match 55.3%; Score 42; DB 2; Length 350;

Best Local Similarity 46.2%; Pred. No. 12;

Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 13

Db 20 YNGRKIFDFTERD 32

RESULT 10

T09378

hypothetical protein F23K16.250 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 01-Dec-2000

C:Accession: T09378; T04999

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16652

A:Accession: T09378

A:Molecule type: DNA

A:Residues: 1-563 <BEV>

A:Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.250

A:Experimental source: cultivar Columbia; BAC clone F23K16

R:Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.W

submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15394

A:Accession: T04999

A:Molecule type: DNA

A:Residues: 444-563 <BE2>

A:Cross-references: EMBL:AL022605

A:Experimental source: cultivar Columbia; BAC clone T19P19

C:Genetics:

A:Gene: ATSP:F23K16.250

A:Map position: 4
A:Introns: 118/3; 502/3
A:Note: T19P19.10

Query Match 55.3%; Score 42; DB 2; Length 563;
Best Local Similarity 58.3%; Pred. No. 21;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13
|||:| |||
Db 491 GGNQLTEFQDKD 502

RESULT 11

C86705
hypothetical protein ygdA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C86705

R;Bolotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: C86705

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-185 <STO>

A:Cross-references: GB:AE005176; PID:g12723547; PIDN:AAK04741.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: ygdA

Query Match 53.9%; Score 41; DB 2; Length 185;
Best Local Similarity 53.6%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGHQIYQFTDKD 13
|||:| |||
Db 154 GHDFYVFTDAD 164

RESULT 12

T21690

hypothetical protein F33A8.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T21690

R;Matthews, L.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19459

A:Accession: T21690

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-467 <WIL>

A:Cross-references: EMBL:Z81525; PIDN:CAB04258.1; GSPDB:GN00020; CESP:F33A8.4

A:Experimental source: clone F33A8

C:Genetics:

A:Gene: CESP:F33A8.4

A:Map position: 2

A:Introns: 29/3; 159/2; 212/3; 243/3; 266/3; 365/3

C:Superfamily: Caenorhabditis elegans hypothetical protein F33A8.4

Query Match 53.9%; Score 41; DB 2; Length 467;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 12
| |||:| :|
Db 368 YEGHKLYQHSEK 379

RESULT 13

D89775

hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89775

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: D89775

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-514 <KUR>

A:Cross-references: GB:BA000018; PID:g13700060; PIDN:BA841359.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA0139

Query Match 53.9%; Score 41; DB 2; Length 514;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13
|||:| |||
Db 449 GGRQIGQFSSKD 460

RESULT 14

G83445

conserved hypothetical protein PA1607 [imported] - Pseudomonas aeruginosa (strain PAO
C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: G83445

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: G83445

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-146 <STO>

A:Cross-references: GB:AE004588; GB:AE004091; MID:g9947563; PIDN:AAG04996.1; GSPDB:GN

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA1607

Query Match 52.6%; Score 40; DB 2; Length 146;

Best Local Similarity 63.6%; Pred. No. 11;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 12
| |||:| |||
Db 75 GSHQYRLTDK 85

RESULT 15

H71979

probable type II restriction enzyme - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C:Accession: H71979

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.

; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: H71979

A:Status: preliminary

A:Molecule type: DNA

A;Residues: 1-260 <ARN>
A;Cross-references: GB:AE001444; GB:AE001439; NID:g4154549; PIDN:AAD05628.1; PID:g415455
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0046

Query Match 52.6%; Score 40; DB 2; Length 260;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTD 11
Db :||||| |||
194 FGGHQAQFND 204

Search completed: October 14, 2003, 08:40:48
Job time : 10.3854 secs

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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:35:36 ; Search time 4.13636 Seconds
(without alignments)
147.798 Million cell updates/sec

Title: US-09-931-700-2

Perfect score: 76

Sequence: 1 YGGHQYQFTDKD 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	57	75.0	185	ADML_HUMAN	P35318 homo sapien
2	57	75.0	185	ADML_RAT	P43145 rattus norv
3	57	75.0	188	ADML_PIG	P33366 sus scrofa
4	52	68.4	188	ADML_BOVIN	O62827 bos taurus
5	52	68.4	188	ADML_CANFA	O77559 canis famil
6	51	67.1	184	ADML_MOUSE	P97297 mus musculu
7	45.5	59.9	980	SYN_DROME	O24546 drosophila
8	39	51.3	425	SYN_METTH	O26346 methanobact
9	39	51.3	705	PPCE_FLAME	P27028 flavobacter
10	39	51.3	1356	ROM2_YEAST	P51862 saccharomyc
11	38	50.0	422	TRSU_PYRKO	P58502 pyrococcus
12	38	50.0	532	CDPK_DAUCA	P28582 daucus caro
13	38	50.0	1337	DEXT_STRDO	P39653 streptococc
14	37.5	49.3	569	AMY_STRVL	P22998 streptomyc
15	37	48.7	257	HIS6_VIBCH	O9ksw8 vibrio chol
16	37	48.7	302	SI7D_HUMAN	O9h4f1 h alpha-n-a
17	37	48.7	360	SI7D_MOUSE	O9r2b6 mus musculu
18	37	48.7	367	I205_MYCTU	O53656 mycobacteri
19	37	48.7	424	CBPT_THEVU	P29068 thermoactin
20	37	48.7	463	SAHF_CAUCR	O9ab08 caulobacter
21	37	48.7	464	DNAA_TREPA	O83047 treponema p
22	37	48.7	628	SNXL_HUMAN	O96rf0 homo sapien
23	37	48.7	632	ETFD_SCHPO	P87111 s probable
24	37	48.7	644	YNLS_YEAST	P53925 saccharomyc
25	37	48.7	663	GRIA_BACCE	O85467 bacillus ce
26	37	48.7	1059	IY379_HUMAN	O15084 homo sapien
27	37	48.7	1071	TRI_THEAC	P50270 streptomyc
28	36.5	48.0	566	AMY_STRGR	O96086 thermoplasma
29	36.5	48.0	566	AMY_STRLM	P09794 streptomyc
30	36	47.4	102	VATE_DESSY	O06503 desulfuroco
31	36	47.4	158	YKFG_ECOLI	O47685 escherichia
32	36	47.4	160	YFJY_ECOLI	P52140 escherichia
33	36	47.4	306	UL31_HSV11	P10215 herpes simp

34	36	47.4	493	1	MUEL_OCEIH	Q8cz66 oceanobacil
35	36	47.4	606	1	ACEA_MYCLE	P46831 mycobacteri
36	36	47.4	608	1	GLMS_SAUTI	Q8z2q2 s glucosami
37	36	47.4	640	1	RAEP_CANAL	O93831 candida alb
38	36	47.4	1557	1	OSP_DROME	O27421 drosophila
39	35.5	46.7	281	1	Y149_MYGE	P47395 mycoplasma
40	35	46.1	136	1	PSBR_TORAC	Q40519 nicotiana t
41	35	46.1	138	1	PSBR_HORVU	Q40070 hordeum vul
42	35	46.1	140	1	PSBR_SPIOL	P10690 spinacia ol
43	35	46.1	209	1	CBFA_PETMA	P25210 petromyzon
44	35	46.1	222	1	THIE_BAGSU	P39594 bacillus su
45	35	46.1	240	1	SFSA_SULSO	Q97vp5 sulfolobus

ALIGNMENTS

RESULT 1
ADML_HUMAN
ID ADML_HUMAN STANDARD; PRT; 185 AA.
AC P35318;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)]
GN ADM OR AM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Phochromocytoma;
RX MEDLINE=93343928; PubMed=7688224;
RA Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
RT "Cloning and characterization of cDNA encoding a precursor for human
adrenomedullin";
RL Biochem. Biophys. Res. Commun. 194:720-725(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94354869; PubMed=8074714;
RA Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuo H.,
RT Kitamura K., Eto T., Matsuo H.;
RL "Genomic structure of human adrenomedullin gene";
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltun E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 95-146.

```

FT  VARIANT      50      S -> R (in dbSNP:5005).
SQ  SEQUENCE      185 AA;  20420 MW;  64C7D2A0B4654DFE CRC64;
                                     /FTId=VAR_014861.
Query Match      75.0%;  Score 57;  DB 1;  Length 185;
Best Local Similarity 100.0%;  Pred.No. 0.0068;
Matches 10;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  4 HQIYQFTDKD 13
Db  122 HQIYQFTDKD 131

RESULT 2
ADML_RAT
ID ADML_RAT STANDARD; PRT; 185 AA.
AC P43145;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (PROAM-N20) (PROAM N-terminal 20 peptide) (PAMP)].
DE ADM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RR STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX MEDLINE=93384621; PubMed=7690563;
RA Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
RA Matsuo H., Eto T.;
RA "Molecular cloning and biological activities of rat adrenomedullin, a
RA hypotensive peptide.";
RA Biochem. Biophys. Res. Commun. 195:921-927(1993).
RN [2]
RP SEQUENCE FROM N.A.
RR TISSUE=Brain;
RX MEDLINE=96102137; PubMed=8524787;
RA Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
RA Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
RA "Discovery of adrenomedullin in rat ischemic cortex and evidence for
RA its role in exacerbating focal brain ischemic damage.";
RA Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
RX [-] FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
AGENTS.
CC CC
CC [-] SUBCELLULAR LOCATION: Secreted.
CC CC
CC [-] TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY,
CC CC HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
CC CC [-] SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC CC
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CC
CC EMBL; D15069; BAA03665.1; -;
CC EMBL; U15419; AAB60519.1; -;
CC PIR; JN0766; JN0766.
CC InterPro; IPR001710; Adrenomedullin.
CC Pfam; PF02039; Adrenomedullin; 1.
CC PRINTS; PR00801; Adrenomedullin.
CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
CC SIGNAL 1 21
CC PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
CC PROPEP 45 91
CC BY SIMILARITY.
CC PEPTIDE 94 143
CC ADRENOMEDULLIN.
CC PROPEP 149 185
CC BY SIMILARITY.
CC PREFRAM C-TERMINAL FRAGMENT (BY
CC SIMILARITY).

```

FT DISULFID 107 112 BY SIMILARITY.
 FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT MOD_RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 SQ SEQUENCE 185 AA; 20636 MW; 35CAD9A9DD19AE35 CRC64;
 Query Match 75.0%; Score 57; DB 1; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0068;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
 |||||
 Db 119 HQIYQFTDKD 128

RESULT 3
 ADML_PIG STANDARD; PRT; 188 AA.
 AC P53366;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM OR AM.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Adrenal medulla;
 RX MEDLINE=94139945; PubMed=8043068;
 RA Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
 RA Kawamoto M., Minamino N., Matsuo H., Eto T.;
 RT "Complete amino acid sequence of porcine adrenomedullin and cloning
 RT of cDNA encoding its precursor.";
 RL FEBS Lett. 338:306-310(1994).
 RN [2]
 RP SEQUENCE OF 22-41.
 RC TISSUE-Adrenal medulla;
 RX MEDLINE=94357274; PubMed=8076689;
 RA Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
 RA Kawamoto M., Minamino N., Matsuo H., Eto T.;
 RT "Identification and hypotensive activity of proadrenomedullin
 RT N-terminal 20 peptide (PAMP).";
 RL FEBS Lett. 351:35-37(1994).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
 CC KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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 DR EMBL; D14875; BAA03590.1; -
 DR PIR; S41600; S41600.
 DR InterPro; IPR001710; Adrenomedullin.
 DR Pfam; PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; Adrenomedullin.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PEPTIDE 45 92
 FT PEPTIDE 95 146
 FT PROPEP 153 188
 FT PREPROAM C-TERMINAL FRAGMENT (BY

FT DISULFID 110 115 BY SIMILARITY.
 FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP).
 FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 188 AA; 20893 MW; 71749460F5660A61 CRC64;
 Query Match 75.0%; Score 57; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
 |||||
 Db 122 HQIYQFTDKD 131

RESULT 4
 ADML_BOVIN STANDARD; PRT; 188 AA.
 AC O62827;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Aorta;
 RX MEDLINE=98244567; PubMed=9585168;
 RA Baker S., Wood E., Clark A.J.L., Corder R.;
 RT "Cloning of bovine proadrenomedullin and inhibition of its basal
 RT expression in vascular endothelial cells by staurosporine.";
 RL Life Sci. 62:1407-1415(1998).
 CC -1- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
 CC CIRCULATION CONTROL (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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 CC -----
 DR EMBL; AJ001613; CAA04866.1; -
 DR InterPro; IPR001710; Adrenomedullin.
 DR Pfam; PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; Adrenomedullin.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PEPTIDE 45 92
 FT PEPTIDE 95 146
 FT PROPEP 148 188
 FT PREPROAM C-TERMINAL FRAGMENT (BY
 FT SIMILARITY).
 FT DISULFID 110 115
 FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 SQ SEQUENCE 188 AA; 20981 MW; 3002E79AB3B6612C CRC64;
 Query Match 68.4%; Score 52; DB 1; Length 188;
 Best Local Similarity 90.0%; Pred. No. 0.052;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 Db 122 HQIYHFTDKD 131

RESULT 5
 ADML_CANFA STANDARD; PRT; 188 AA.
 AC 07759; Q9TWC9;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Imoto I., Jougasaki M.;
 RT "Cloning of cDNA encoding canine adrenomedullin.";
 RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99002704; PubMed=9788655;
 RA Ono Y., Kojima M., Okada K., Kangawa K.;
 RT "cDNA cloning of canine adrenomedullin and its gene expression in the
 RT heart and blood vessels in endotoxin shock.";
 RT Shock 10:243-247(1998).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
 CC
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 CC
 CC EMBL; AF045773; AAD05423.1; -
 DR EMBL; U96127; RAD09957.1; -
 DR InterPro: IPR001710; Adrenomedullin.
 DR Pfam; PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; ADRENOMEDULLIN.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PROPEP 45 92 BY SIMILARITY.
 FT PEPTIDE 95 146 ADRENOMEDULLIN.
 FT PROPEP 148 188 PREPROAM C-TERMINAL FRAGMENT (BY
 FT SIMILARITY).
 FT FT BY SIMILARITY.
 FT FT AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT FT AMIDATION (G-147 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT FT N -> K (IN REF. 2).
 SQ SEQUENCE 188 AA; 20929 MW; 809D6A64F98F5578 CRC64;
 Query Match 58.4%; Score 52; DB 1; Length 188;
 Best Local Similarity 90.0%; Pred. No. 0.052;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 Db 122 HQIYQFTDND 131

RESULT 6
 ADML_MOUSE STANDARD; PRT; 184 AA.
 AC P97297; P97453;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=129/Sv;
 RX MEDLINE=97092892; PubMed=8938454;
 RA Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
 RA Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
 RT "Genomic organization, expression, and chromosomal mapping of the
 RT mouse adrenomedullin gene.";
 RL Genomics 37:395-399(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J;
 RX MEDLINE=99046755; PubMed=9808778;
 RA Yotsumoto S., Shimada T., Cui C.Y., Nakashima H., Fujiwara H.,
 RA Ko M.S.H.;
 RT "Expression of adrenomedullin, a hypotensive peptide, in the
 RT trophoblast giant cells at the embryo implantation site in mouse.";
 RL Dev. Biol. 203:264-275(1998).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
 CC
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 CC
 CC EMBL; D78349; EAA11367.1; -
 DR EMBL; U77630; AAB36535.1; -
 DR MGD; MGI:108058; Agm.
 DR InterPro: IPR001710; Adrenomedullin.
 DR Pfam; PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; ADRENOMEDULLIN.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PROPEP 45 92 BY SIMILARITY.
 FT PEPTIDE 95 144 ADRENOMEDULLIN.
 FT PROPEP 151 184 PREPROAM C-TERMINAL FRAGMENT (BY
 FT SIMILARITY).
 FT FT BY SIMILARITY.
 FT FT AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT FT AMIDATION (G-145 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT FT A -> G (IN REF. 2).
 SQ SEQUENCE 184 AA; 20764 MW; C88C99045A79C898 CRC64;
 Query Match 67.1%; Score 51; DB 1; Length 184;
 Best Local Similarity 90.0%; Pred. No. 0.076;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 Db 120 HQIYQLTDKD 129


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RESULT 7
SYN_DROME
ID SYN_DROME STANDARD; PRT; 980 AA.
AC Q24546; Q24545;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Synapsin.
GN SYN OR SYN1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS SYN-S AND SYN1-RT).
RC STRAIN=Berlin; TISSUE=Head;
RX MEDLINE=96209149; PubMed=8627354;
RA Klages B.R.E., Heimbeck G., Godenschwege T.A., Hofbauer A.,
RA Pflugfelder G.O., Reifegerste R., Reisch D., Schaupp M., Buchner S.,
RA Buchner E.
RT "Invertebrate synapsins: a single gene codes for several isoforms in
Drosophila."
RL J. Neurosci. 16:3154-3165(1996).
CC -!- SUBCELLULAR LOCATION: SYNAPSE.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name-Syn1-RT;
CC isoId=Q24546-1; Sequence=Displayed;
CC Name-Syn-S;
CC isoId=Q24546-2; Sequence=VSP_006324;
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE NERVOUS SYSTEM.
CC -!- SIMILARITY: BELONGS TO THE SYNAPSIN FAMILY.
CC -----
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CC -----
CC EMBL; X95453; CAA64723.1; -.
CC EMBL; X95453; CAA64722.1; -.
CC HSSP; P17599; 1AUX.
CC FlyBase; FBgn0004575; Syn.
CC InterPro; IPR001359; Synapsin.
CC Pfam; PF02078; Synapsin; 1.
CC Pfam; PF02750; Synapsin_C; 1.
CC PRINTS; PR01368; SYNAPSIN.
CC PROSITE; PS00415; SYNAPSIN_1; FALSE NEG.
CC PROSITE; PS00416; SYNAPSIN_2; FALSE NEG.
CC Synapse; Neurone; Alternative splicing.
CC DOMAIN 2 7 POLY-PRO.
CC DOMAIN 668 680 POLY-SER.
CC DOMAIN 692 695 POLY-PRO.
CC DOMAIN 698 703 POLY-PRO.
CC VARSPLIC 539 980 Missing (in isoform Syn-S).
CC FTID=VSP_006324.
CC FTID=VSP_006324.
CC SEQUENCE 980 AA; 102799 MW; E6037A2A4604F944 CRC64;

Query Match 59.9%; Score 45.5; DB 1; Length 980;
Best Local Similarity 52.6%; Pred. No. 4;
Matches 10; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 1 YGG-----HQIYQFTDK 12
||| |
Db 181 YGGVPSINSLSHYQFDK 199

RESULT 8

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SYN_METTH
ID SYN_METTH STANDARD; PRT; 425 AA.
AC Q26346;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
DE (HISRS).
GN HISS OR MTH244.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Hashizadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiواني N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shiner G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT J. Bacteriol. 179:7135-7155(1997).
CC -!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) -> AMP +
CC diphosphate + L-histidyl-tRNA(His).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC -----
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CC -----
CC EMBL; AE000811; AAB84750.1; ALT_INIT.
CC HSSP; O32422; IQE0.
CC HAMAP; MF_00127; -.
CC InterPro; IPR004154; HGTP-anticonodon.
CC InterPro; IPR004516; HISS.
CC InterPro; IPR002314; tRNA-synt_2b.
CC InterPro; IPR006195; tRNA_ligase_II.
CC Pfam; PF03129; HGTP-anticonodon; 1.
CC Pfam; PF00587; tRNA-synt_2b; 1.
CC TIGRFAMS; TIGR00442; hiss; 1.
CC PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SEQUENCE 425 AA; 48019 MW; 8388A5975A017535 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 425;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 HQIYQFTDK 12
:|||||
Db 60 NQIYHFTDK 68

RESULT 9
PPCE_FLAME
ID PPCE_FLAME STANDARD; PRT; 705 AA.
AC P27028;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Prolyl endopeptidase precursor (EC 3.4.21.26) (Proline-specific
DE endopeptidase) (PSE) (post-proline cleaving enzyme) (PE).

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GN FlPEP1.
OS Flavobacterium meningosepticum (Chryseobacterium meningosepticum).
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Chryseobacterium.
OX NCBI_TaxID=238;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92176159; PubMed=1840588;
RA Yoshimoto T., Kanatani A., Shinoda T., Inaoka T., Kokubo T., Tsuru D.;
RT "Prolyl endopeptidase from Flavobacterium meningosepticum: cloning
RT and sequencing of the enzyme gene.";
RT J. Biochem. 110:873-878(1991).
RN [2]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=94114173; PubMed=7764331;
RA Dietenthal T., Dargatz H., Witte V., Reipen G., Svendsen I.;
RT "Cloning of proline-specific endopeptidase gene from Flavobacterium
RT meningosepticum: expression in Escherichia coli and purification of
RT the heterologous protein.";
RL Appl. Microbiol. Biotechnol. 40:90-97(1993).
CC -!- FUNCTION: CLEAVES PEPTIDE BONDS ON THE C-TERMINAL SIDE OF PROLYL
CC RESIDUES WITHIN PEPTIDES THAT ARE UP TO APPROXIMATELY 30 AMINO
CC ACIDS LONG. HAS AN ABSOLUTE REQUIREMENT FOR AN X-PRO BOND IN THE
CC TRANS CONFIGURATION IMMEDIATELY PRECEDING THE PRO-Y SCISSIBLE
CC BOND.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of Pro-Xaa >> Ala-Xaa in
CC oligopeptides.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9A.
CC
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CC
CC EMBL; D10980; BAA01755.1; -.
CC EMBL; X63674; CAA45213.1; -.
CC PIR; JX0194; JX0194.
CC HSP; P23687; IQFM.
CC MEROPS; S09.001; -.
CC InterPro; IPR001375; Peptidase_S9.
CC InterPro; IPR004106; Peptidase_S9_N.
CC InterPro; IPR002471; Prol_endopep_ser.
CC InterPro; IPR002470; Proligo_Ptase.
CC InterPro; IPR000379; Ser_estr_site.
CC Pfam; PF00326; Peptidase_S9; 1.
CC Pfam; PF02897; Peptidase_S9_N; 1.
CC PRINTS; PR00852; PROLIGOPTASE.
CC PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
KW Hydrolase; Serine protease; Periplasmic; Signal.
FT SIGNAL 1 20
FT CHAIN 21 705 PROLYL ENDOPEPTIDASE.
FT ACT_SITE 556 556 CHARGE RELAY SYSTEM.
FT ACT_SITE 675 675 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CONFLICT 110 110 S -> C (IN REF. 2).
FT CONFLICT 587 587 R -> A (IN REF. 2).
SQ SEQUENCE 705 AA; 78707 MW; BCUEDCBAB328256 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 705;
Best Local Similarity 63.6%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GHQIYQFTDKD 13
| : | | | | |
DB 306 GDTLVLFYTDKD 316

RESULT 10
ROM2_YEAST

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ID ROM2_YEAST STANDARD; PRT; 1356 AA.
AC P51862;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE RH01 GDP-GTP exchange protein 2.
GN ROM2 OR YLR371W OR L8039.3.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansoerge W.,
RA Benes V., Bruckner M., Delius H., Dubois E., Duesterhoef A.,
RA Entian K.-D., Floeth M., Goifeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohelsel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
RN [2]
RN CHARACTERIZATION.
RX MEDLINE=96208506; PubMed=8641285;
RA Ozaki K., Tanaka K., Imamura H., Hihara T., Kameyama T.,
RA Nonaka H., Hirano H., Matsura Y., Takai Y.;
RT "Rom1p and Rom2p are GDP/GTP exchange proteins (GEPs) for the Rholf
RT small GTP binding protein in Saccharomyces cerevisiae.";
RL EMBO J. 15:2196-2207(1996).
CC -!- FUNCTION: STIMULATES THE EXCHANGE OF RH01 GDP-BOUND FORM INTO
CC GTP-BOUND FORM.
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC
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CC
CC EMBL; U19103; AAB67564.1; -.
CC PIR; S51389; S51389.
CC SGD; S0004363; ROM2.
CC GO; GO:0005934; C:bud tip; IDA.
CC GO; GO:0005089; F:rho guanyl-nucleotide exchange factor activity; IDA.
CC GO; GO:0004871; F:signal transducer activity; IPI.
CC GO; GO:0007117; P:bud growth; IPI.
CC GO; GO:0007047; P:cell wall organization and biogenesis; IPI.
CC GO; GO:0000283; P:establishment of cell polarity (sensu Sacch.); IPI.
CC GO; GO:0007264; P:small GTPase mediated signal transduction; IPI.
CC InterPro; IPR001180; Citron.
CC InterPro; IPR000591; DEP.
CC InterPro; IPR001331; GDS_CDC24.
CC InterPro; IPR000219; RhoGEF.
CC Pfam; PF00780; CNH; 1.
CC Pfam; PF00610; DEP; 1.
CC Pfam; PF00621; RhoGEF; 1.
CC SMART; SM00036; CNH; 1.
CC SMART; SM00049; DEP; 1.
CC SMART; SM00325; RhoGEF; 1.
CC PROSITE; PS00741; DH_1; FALSE_NEG.
CC PROSITE; PS00101; DH_2; 1.
KW Guanine-nucleotide releasing factor.
FT DOMAIN 659 846 DH.
FT DOMAIN 252 265 POLY-ASN.

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FT DOMAIN 329 336 POLY-RIS.
 FT DOMAIN 632 635 POLY-ASP.
 SQ SEQUENCE 1356 AA; 152595 MW; 5FBC542114E7BC92 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 1356;
 Best Local Similarity 62.5%; Pred. No. 78;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOIYQFTD 11
 |:::|
 Db 496 HEVIEFTD 503

RESULT 11
 ID TKSU_PYRKO STANDARD; PRT; 422 AA.
 AC P58502; Q977F5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE TK-subtilisin precursor (EC 3.4.21.-).
 OS Pyrococcus kodakarensis.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Thermococcus.
 OX NCBI_TaxID=69014;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=KOD1;
 RX MEDLINE=21266834; PubMed=11375149;
 RA Kannan Y., Koga Y., Inoue Y., Haruki M., Takagi M., Imanaka T.,
 RA Morikawa M., Kanaya S.;
 RT "Active subtilisin-like protease from a hyperthermophilic archaeon in
 a form with a putative prosequence";
 RL Appl. Environ. Microbiol. 67:2445-2452(2001).
 CC -1- FUNCTION: Has a broad substrate specificity with a slight
 preference to large hydrophobic amino acid residues at the P1
 position.
 CC -1- COFACTOR: Calcium.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: Thermostable; high activity at 80 degrees Celsius.
 CC -1- OPTIMAL pH is 9.5.
 CC -1- SIMILARITY: Belongs to peptidase family S8.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AB056701; BAB60701.1;
 CC InterPro: IPR000209; Peptidase_S8.
 CC Pfam: PF00082; Peptidase_S8; 1.
 CC PRINTS: PR00723; SUBTILISIN.
 CC PROSITE: PS00136; SUBTILASE_ASP; 1.
 CC PROSITE: PS00138; SUBTILASE_SER; 1.
 KW Hydrolase; Serine protease; Calcium-binding; Zymogen; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT PROPEP 25 106 POTENTIAL.
 FT CHAIN 107 422 TK-SUBTILISIN.
 FT ACT_SITE 139 139 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 177 177 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 348 348 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 422 AA; 43785 MW; 843255BCD806DB71 CRC64;

Query Match 50.0%; Score 38; DB 1; Length 422;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHQYQF 9
 |:::|

Db 50 GGHVYQF 57

RESULT 12
 ID CDPK_DAUCA STANDARD; PRT; 532 AA.
 AC P28582;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calcium-dependent protein kinase (EC 2.7.1.-) (CDPK).
 OS Daucus carota (Carrot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; campanulids; Apiales; Apiaceae; Daucus.
 OX NCBI_TaxID=4039;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choi J.H.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 108-532 FROM N.A.
 RX MEDLINE=92003674; PubMed=1912486;
 RA Suen K.-L., Choi J.H.;
 RT "Isolation and sequence analysis of a cDNA clone for a carrot
 calcium-dependent protein kinase: homology to
 calcium/calmodulin-dependent protein kinases and to calmodulin.";
 RL Plant Mol. Biol. 17:581-590(1991).
 CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
 INVOLVE CALCIUM AS A SECOND MESSENGER.
 CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
 PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X56599; CAA39936.1;
 CC PIR: S17759; S17759.
 CC PIR: T14335; T14335.
 CC HSSP: G63450; 1A06.
 CC InterPro: IPR002048; EF-hand.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_pkinase.
 CC Pfam: PF00036; ehand; 4.
 CC Pfam: PF00069; pkinase; 1.
 CC ProDom: PD000012; EF-hand; 2.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SM00054; EFh; 4.
 CC SMART: SM00220; S_TKc; 1.
 CC PROSITE: PS0018; EF_HAND; 4.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC Calcium-binding; Phosphorylation.
 FT DOMAIN 81 339 PROTEIN KINASE.
 FT BINDING 87 95 ATP (BY SIMILARITY).
 FT BINDING 110 110 ATP (BY SIMILARITY).
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT CA_BIND 395 406 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 431 442 EF-HAND 2 (POTENTIAL).
 FT CA_BIND 465 476 EF-HAND 3 (POTENTIAL).
 FT CA_BIND 500 511 EF-HAND 4 (POTENTIAL).
 SQ SEQUENCE 532 AA; 60065 MW; F03E6F036A0AE348 CRC64;

Query Match 50.0%; Score 38; DB 1; Length 532;
 Best Local Similarity 60.0%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 ||:|:|:|
 DB 458 HQAFQYFDKD 467

RESULT 13

DEXT_STROD STANDARD; PRT: 1337 AA.
 AC P3953;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-glucanohydrolase).
 GN DEX.
 OS Streptococcus downei (Streptococcus sobrinus).
 OG Plasmid pYA902.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1317;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-36.
 RC STRAIN=6715 / UAB66;
 RX MEDLINE=94292401; PubMed=8021165;
 RA Wanda S.-Y., Curtiss R. III;
 RT "Purification and characterization of Streptococcus sobrinus dextranase produced in recombinant Escherichia coli and sequence analysis of the dextranase gene."
 RT J. Bacteriol. 176:3839-3850(1994).
 RL -!- FUNCTION: MAY PLAY A ROLE IN SUCROSE-INDEPENDENT ADHERENCE TO THE PELLICULE-COATED TOOTH SURFACE.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic linkages in dextran.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
 CC -!- MISCELLANEOUS: The activity of this enzyme is optimal at pH 5.3 and at 39 degrees Celsius.
 CC -!- SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
 CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
 CC
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 CC
 CC EMBL; M96978; AAA21772.1; ..
 CC InterPro; IPR001899; Gram_pos_anchor.
 CC InterPro; IPR006192; LPXTG.
 CC Pfam; PF00746; Gram_pos_anchor; 1.
 CC TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 CC PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 CC Hydrolase; Glycosidase; Cell wall; Peptidoglycan-anchor; Repeat;
 KW Signal; Plasmid.
 FT SIGNAL 1 30
 FT CHAIN 31 1308 DEXTRANASE.
 FT PROPEP 1309 1337 REMOVED BY SORTASE (POTENTIAL).
 FT SITE 1305 1309 LPXTG SORTING SIGNAL (POTENTIAL).
 FT MOD_RES 1308 1308 AMIDE-LINKED TO CELL WALL (POTENTIAL).
 SQ SEQUENCE 1337 AA; 143298 MW; B494275A77A2E3D0 CRC64;

Query Match 50.0%; Score 38; DB 1; Length 1337;
 Best Local Similarity 41.7%; Pred. No. 11e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHIYQFTDKD 13

DB 457 GDNEVSYADKD 468
 ||:|:|:|

RESULT 14

AMY_STRVL STANDARD; PRT: 569 AA.
 AC P2298;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
 GN AML.
 OS Streptomyces violaceus (Streptomyces venezuelae).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1936;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15068;
 RX MEDLINE=89232724; PubMed=3266752;
 RA Virolle M.-J., Long C.M., Chang S., Bibb M.J.;
 RT "Cloning, characterization and regulation of an alpha-amylase gene from Streptomyces venezuelae."
 RL Gene 74:321-334(1988).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -!- INDUCTION: BY MALTOSE, AND REPRESSION BY GLUCOSE.
 CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC
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 CC
 CC EMBL; M25263; AAB36561.1; ..
 CC PIR; JS0101; JS0101.
 CC HSP; P29957; IAQM.
 CC InterPro; IPR006589; Alp_amyl_cat_sub.
 CC InterPro; IPR006048; Alpha_amyl_C.
 CC InterPro; IPR006047; Alpha_amyl_cat.
 CC InterPro; IPR002044; CBD_4.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; alpha-amylase; 1.
 CC Pfam; PF02806; alpha-amylase_C; 1.
 CC Pfam; PF00686; CBM_20; 1.
 CC PRINTS; PR00110; ALPHAAMYLASE.
 CC PRODOM; PD001568; CBD_4; 1.
 CC SMART; SM00642; Amy; 1.
 CC SMART; SM00632; Amy_C; 1.
 CC Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
 KW SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 569 ALPHA-AMYLASE.
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT ACT_SITE 209 209 BY SIMILARITY.
 FT ACT_SITE 296 296 BY SIMILARITY.
 SQ SEQUENCE 569 AA; 60637 MW; 14CA5BD56720043 CRC64;

Query Match 49.3%; Score 37.5; DB 1; Length 569;
 Best Local Similarity 50.0%; Pred. No. 58;
 Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 YGG---HQIYQFTDKD 13
 ||:|:|:|
 DB 324 YGSPDVHSGYEWTDKD 339

RESULT 15

Job time : 7.13636 secs

```
HIS6_VIBCH
ID HIS6_VIBCH STANDARD; PRT; 257 AA.
AC C9KSW8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGP
DE synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase
DE subunit hisF) (IGPS subunit hisF).
GN HISF OR VC1138.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unwayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Niernan W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
CC -!- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to
CC IGP, AICAR and glutamate. The hisF subunit catalyzes the
CC cyclization activity that produces IGP and AICAR from PRFAR using
CC the ammonia provided by the hisH subunit (By similarity).
CC -!- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-
CC ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
CC carboxamide + L-glutamine -> imidazole-glycerol phosphate + 5-
CC aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC -!- PATHWAY: Histidine biosynthesis; fifth step.
CC -!- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE HISA / HISF FAMILY.
CC -----
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CC -----
CC EMBL; AE004193; AAF94297.1; -.
CC PIR; E82238; E82238.
CC TIGR; VC1138; -.
CC HAMAP; MF_01013; -.
CC InterPro; IPR003009; FMN_enzyme.
CC InterPro; IPR006062; His_biosynth.
CC InterPro; IPR004651; HisF.
CC Pfam; PF00977; His_biosynth; 1.
CC TIGRFAMs; TIGR00735; hisF; 1.
KW Histidine biosynthesis; lyase; Complete proteome.
FT ACT_SITE 11 11
FT ACT_SITE 130 130
FT ACT_SITE 130 130
SQ SEQUENCE 257 AA; 28338 MW; F722BBC43BEE153C CRC64;

Query Match 48.7%; Score 37; DB 1; Length 257;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHQIQFT 10
Db 138 GQYQYQFT 146
```

Search completed: October 14, 2003, 08:39:09

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:36:06 ; Search time 17.4318 Seconds
(without alignments)
192.446 Million cell updates/sec

Title: US-09-931-700-2

Perfect score: 76
Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	57	75.0	27	6 Q9TRZ6	Q9trz6 sus scrofa
2	52	68.4	188	6 Q95KP0	Q95kp0 bos taurus
3	51	67.1	643	16 Q55549	Q55549 synchocyst
4	45.5	59.9	348	5 Q81NM4	Q81nm4 drosophila
5	45.5	59.9	388	5 Q24544	Q24544 drosophila
6	45.5	59.9	443	5 Q9VH15	Q9vh15 drosophila
7	45.5	59.9	537	5 Q81NM6	Q81nm6 drosophila
8	45	59.2	776	10 Q81050	Q81050 arabidopsis
9	44	57.9	514	2 Q9XSR9	Q9xsr9 streptomyce
10	44	57.9	2231	16 Q9ZKK7	Q9zkk7 helicobacte
11	42	55.3	173	5 Q8MXJ0	Q8mxj0 caenorhabdi
12	42	55.3	184	16 Q9EWQ4	Q9ewq4 streptomyce
13	42	55.3	280	16 Q45612	Q45612 bacillus su
14	42	55.3	324	16 Q9A5R9	Q9a5r9 caulobacter
15	42	55.3	326	16 Q8RCV8	Q8rcv8 thermoanaer
16	42	55.3	350	5 Q19582	Q19582 caenorhabdi

17	42	55.3	563	10 Q9SV96	Q9sv96 arabidopsis
18	42	55.3	1206	3 Q9UT2	Q9uti2 schizosacch
19	41	53.9	185	2 Q9L474	Q9l474 lactococcus
20	41	53.9	185	16 Q9CHS8	Q9chs8 lactococcus
21	41	53.9	467	5 Q62214	Q62214 caenorhabdi
22	41	53.9	514	16 Q99X71	Q99x71 staphylococ
23	41	53.9	514	16 Q8NVQ7	Q8nvq7 staphylococ
24	40.5	53.3	466	5 Q76322	Q76322 loligo peal
25	40.5	53.3	503	5 Q76323	Q76323 loligo peal
26	40	52.6	106	4 Q9UGX0	Q9ugx0 homo sapien
27	40	52.6	146	16 Q913B4	Q913b4 pseudomonas
28	40	52.6	229	2 Q8VTE0	Q8vte0 helicobacte
29	40	52.6	260	16 Q9ZN14	Q9zn14 helicobacte
30	40	52.6	261	2 Q8VTB6	Q8vtb6 helicobacte
31	40	52.6	261	2 Q8VTE3	Q8vte3 helicobacte
32	40	52.6	261	2 Q8VLL3	Q8vll3 helicobacte
33	40	52.6	261	2 Q8VTE5	Q8vte5 helicobacte
34	40	52.6	261	2 Q8VTE8	Q8vte8 helicobacte
35	40	52.6	275	5 Q16622	Q16622 caenorhabdi
36	40	52.6	340	5 Q96512	Q96512 caenorhabdi
37	40	52.6	377	16 Q8KCL8	Q8kcl8 chlorobium
38	40	52.6	470	4 Q9BSU7	Q9bsu7 homo sapien
39	40	52.6	470	11 Q99LFO	Q99lfo mus musculu
40	40	52.6	687	10 Q8S011	Q8s011 oryza sativ
41	40	52.6	769	10 Q943E0	Q943e0 oryza sativ
42	40	52.6	1298	11 Q8CHG6	Q8chg6 mus musculu
43	40	52.6	1841	4 Q15031	Q15031 homo sapien
44	39.5	52.0	606	3 Q9USQ7	Q9usq7 schizosacch
45	39	51.3	95	16 Q8EPG1	Q8epg1 oceanobacil

ALIGNMENTS

RESULT 1

Q9TRZ6					
ID	Q9TRZ6	PRELIMINARY;	PRT;	27 AA.	
AC	Q9TRZ6;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	ADRENOMEDULLIN.				
SUS	Sus scrofa (pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCHI_TaxID=9823;				
RN	[1]				
SEQUENCE	FROM N.A.				
RX	MEDLINE=96157714; PubMed=8576091;				
RA	Ichiki Y., Kitamura K., Kangawa K., Kawamoto M., Matsuo H., Eto T.;				
RT	"Distribution and characterization of immunoreactive adrenomedullin in				
RT	porcine tissue, and isolation of adrenomedullin [26-52] and				
RT	adrenomedullin [34-52] from porcine duodenum.";				
RL	J. Biochem. 118:765-770(1995).				
DR	InterPro; IPR001710; Adrenomedullin.				
DR	Pfam; PF02039; Adrenomedullin; 1.				
DR	PRINTS; PRO0801; ADRENOMEDULLN.				
SQ	SEQUENCE 27 AA; 3063 MW; B8DC7FA18DB3D90 CRC64;				

Query Match 75.0%; Score 57; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13

Db 3 HQIYQFTDKD 12

RESULT 2

Q95KP0					
ID	Q95KP0	PRELIMINARY;	PRT;	188 AA.	
AC	Q95KP0;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Adrenomedullin.
 GN PBAM-2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
 RA Kangawa K., Eto T.;
 RT "ADRENOMEDULLIN (11-26): AN ENDOGENOUS HYPERTENSIVE PEPTIDE ISOLATED
 RT FROM BOVINE ADRENAL MEDULLA.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB055107; BAB62176.1; -;
 DR InterPro: IPR001710; Adrenomedullin.
 DR Pfam: PF02039; Adrenomedullin; 1.
 DR PRINTS; PRO0801; ADRENOMEDULLIN.
 SQ SEQUENCE 188 AA; 20963 MW; 6102E69A756DCA86 CRC64;
 Query Match 68.4%; Score 52; DB 6; Length 188;
 Best Local Similarity 90.0%; Pred. No. 0.54;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 HQIYQFTDKD 13
 Db 122 HQIYHFTDKD 131
 RESULT 3
 Q5549 PRELIMINARY; PRT; 643 AA.
 ID Q5549;
 AC Q5549;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein sir0168.
 GN SIR0168.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 6803;
 RA Tabata S.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome.";
 RL DNA Res. 2:153-166(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D33999; BAA10047.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 643 AA; 68369 MW; 1EE900ID3332B411 CRC64;

Query Match 67.1%; Score 51; DB 16; Length 643;
 Best Local Similarity 72.7%; Pred. No. 3;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GHQIYQFTDKD 13
 Db 447 GHEIYQYTDPD 457
 RESULT 4
 Q8INM4 PRELIMINARY; PRT; 348 AA.
 ID Q8INM4;
 AC Q8INM4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG3985-PC.
 GN SYN.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Hanzon J., An H., Balowin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
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 Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 Stapleton M., Strong R., Svitskas R., Tector C., Tyler D.,
 Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 "Sequencing of Drosophila melanogaster genome.";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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 RN SEQUENCE FROM N.A.
 RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 Radecky P., Huang Y., Kamnik J.S., Procnik S.E., Smith C.D.,
 Tupy J.L., Bergman C., Beriman B., Carlson J.W., Celniker S.E.,
 Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 "Annotation of Drosophila melanogaster genome.";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A.
 RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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 RN SEQUENCE FROM N.A.
 RP FlyBase;
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003686; AAN13464.1; - 8FA837EF9A438134 CRC64;
 SQ SEQUENCE 348 AA; 38221 MW; 8FA837EF9A438134 CRC64;
 Query Match 59.9%; Score 45.5; DB 5; Length 348;
 Best Local Similarity 52.6%; Pred. No. 13;
 Matches 10; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
 QY 1 YGG-----HQIYQFTDK 12
 Db 41 YGGVPSINSLHSIYQFQDK 59
 RESULT 5
 Q24544
 ID Q24544 PRELIMINARY; PRT; 388 AA.
 AC Q24544;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 16, Last annotation update)
 DE Homologous to synapsin II (Fragment).
 GN SYN OR SYN2 OR CG3385.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
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 RC STRAIN=WILDTYPE 'BERLIN'; TISSUE=Head;
 RX MEDLINE=96209149; PubMed=8627354;
 RA Klagges B.R., Heimbeck G., Godenschwege T.A., Hofbauer A.,
 R. pflugfelder G.O., Reifegerste R., Reisch D., Schupp M., Buchner S.,
 Buchner E.;
 RA "Invertebrate synapsins: a single gene codes for several isoforms in
 Drosophila.";
 RT J. Neurosci. 16:3154-3165(1996).
 RL EMBL: X95454; CAA64724.1; -.
 DR HSSP; P17599; 1AUX.
 DR FlyBase; FBgn004575; Syn.
 DR InterPro; IPR001359; Synapsin.
 DR Pfam; PF02078; Synapsin; 1.
 DR Pfam; PF02750; Synapsin_C; 1.
 DR PRINTS; PR01368; SYNAPSIN.
 FT NON_TER 1
 SQ SEQUENCE 388 AA; 42887 MW; 583B24E6456CBF40 CRC64;

Query Match 59.9%; Score 45.5; DB 5; Length 388;
 Best Local Similarity 52.6%; Pred. No. 15;
 Matches 10; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
 QY 1 YGG-----HQIYQFTDK 12
 Db 81 YGGVPSINSLHSIYQFQDK 99
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 Q9VHL5
 ID Q9VHL5 PRELIMINARY; PRT; 443 AA.
 AC Q9VHL5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG3985-PD.
 GN SYN.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
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 Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 Burkova K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
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 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svitskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
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 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
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 Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 Ferreira S., Frise E., Galie R.F., Garg N.S., George R.A.,
 Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Gocayne J.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A0003686; AAF54506.2; -
DR FlyBase; FBgn0004575; Syn.
SQ SEQUENCE 443 AA; 47645 MW; D1B10DA3E655C59D CRC64;
Query Match 59.9%; Score 45.5; DB 5; Length 443;
Best local Similarity 52.6%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
QY 1 YGG-----HQYQFTDK 12
||| |
DB 87 YGGVPSINSLSHSYQFQDK 105
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RESULT 7
Q81NM6 PRELIMINARY; PRT; 537 AA.
AC Q81NM6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CG3985-PB.
GN SYN.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
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RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE FROM N.A.
RP Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
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RA Ferrera S., Frise E., Galie R.F., Garg N.S., George R.A.,
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RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
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RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
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RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A0003686; AAN13462.1; -
SQ SEQUENCE 537 AA; 57691 MW; 782BE20B4BE60220 CRC64;
Query Match 59.9%; Score 45.5; DB 5; Length 537;
Best local Similarity 52.6%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
QY 1 YGG-----HQYQFTDK 12
||| |
DB 181 YGGVPSINSLSHSYQFQDK 199
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RESULT 8
Q81050 PRELIMINARY; PRT; 776 AA.
ID O81050

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AC O81050;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE At2g03240 protein.
GN At2g03240.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10611797;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005313; AAC34478.1; -.
DR InterPro; IPR004342; EXS.Ctcrn.
DR InterPro; IPR004331; SPX.
DR Pfam; PF03124; EXS; 1.
DR Pfam; PF03105; SPX; 1.
SQ SEQUENCE 776 AA; 89775 MW; BE30603ACFADD014E CRC64;

Query Match 59.2%; Score 45; DB 10; Length 776;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13
DB 84 GGHQIGHFSDSD 95

RESULT 9
Q9X5R9
ID Q9X5R9 PRELIMINARY; PRT; 514 AA.
AC Q9X5R9;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MmCA.
GN MmCA.
OS Streptomyces lavendulae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1914;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 2564;
RX MEDLINE=99201491; PubMed=10099135;
RA Mao Y., Varoglu M., Sherman D.H.;
RT "Molecular characterization and analysis of the biosynthetic gene
RT cluster for the antitumor antibiotic mitomycin C from Streptomyces
RT lavendulae NRRL 2564.";
RL Chem. Biol. 6:251-263(1999).
DR EMBL; AF127374; AAD32724.1; -.
SQ SEQUENCE 514 AA; 55697 MW; 888C7E685882E2F CRC64;

Query Match 57.9%; Score 44; DB 2; Length 514;
Best Local Similarity 80.0%; Pred. No. 36;

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Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHQIYQFTD 11
DB 66 GGHQIYQFYD 75

RESULT 10
Q9ZKK7
ID Q9ZKK7 PRELIMINARY; PRT; 2231 AA.
AC Q9ZKK7;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Putative.
GN JHP0928.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., DeJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR EMBL; AB001522; AAD06506.1; -.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR002296; N12N6_mtfrase.
DR InterPro; IPR000330; SNF2_N;
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF00176; SNF2_N; 1.
DR PRINTS; PR00507; N12N6MTFRASE.
DR SMART; SM00487; DEXDc; 1.
DR SMART; SM00490; HELICc; 1.
KW Complete proteome.
SQ SEQUENCE 2231 AA; 255764 MW; 169B86503B7A2A8E CRC64;

Query Match 57.9%; Score 44; DB 16; Length 2231;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGHQIYQFTDKD 13
DB 620 YGNHKIYSSNDKE 632

RESULT 11
Q8MXJ0
ID Q8MXJ0 PRELIMINARY; PRT; 173 AA.
AC Q8MXJ0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein C08G9.1.
GN C08G9.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";

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RL Science 282:2012-2018(1998).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Geisel C., Stellyes L.;
RT "The sequence of *C. elegans* cosmid C08G9.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF036687; AM75374.1; -;
DR WormPep; C08G9.1; CE31155.
KW Hypothetical protein.
SQ SEQUENCE 173 AA; 20056 MW; 2757D83377864CEC CRC64;

Query Match 55.3%; Score 42; DB 5; Length 173;
Best Local Similarity 58.3%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13
||||: |||:
DB 21 GGHQVKCFCDRD 32

RESULT 12

Q9EWQ4 PRELIMINARY; PRT; 184 AA.
AC Q9EWQ4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative lipoprotein.
GN SCO7673 OR SC4C2.08.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Batenham A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";

RL Nature 417:141-147(2002).
DR EMBL: AL939132; CAC17490.1; -;
DR InterPro: IPR005297; Lipoprotein_15.
DR Pfam: PF03640; Lipoprotein_15; 2.
KW Lipoprotein; Complete proteome.
SQ SEQUENCE 184 AA; 19107 MW; 9E532A2748AFDE4A CRC64;

Query Match 55.3%; Score 42; DB 16; Length 184;
Best Local Similarity 54.5%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGHQIYQFTD 11
|||: |||:
DB 134 YNGHPLYRFAD 144

RESULT 13

Q45612 PRELIMINARY; PRT; 280 AA.
AC Q45612;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE YycI protein.
GN YycI.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX Zhang J., Aronson A.I.;
RT "A Bacillus subtilis bglA gene encoding phospho-beta-glucosidase is
RT inducible and closely linked to a NADH dehydrogenase-encoding gene.";
RL Gene 140:85-90(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94156824; PubMed=8113162;
RA Calogero S., Gardan R., Glaser P., Schweizer J., Rapoport G.,
RA Debarbouille M.;
RT "RocR, a novel regulatory protein controlling arginine utilization in
RT Bacillus subtilis, belongs to the NtrC/NifA family of transcriptional
RT activators.";
RL J. Bacteriol. 176:1234-1241(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94236234; PubMed=8180695;
RA Hartford O.M., Dowds B.C.;
RT "Isolation and characterization of a hydrogen peroxide resistant
RT mutant of Bacillus subtilis.";
RL Microbiology 140:297-304(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96093926; PubMed=7584049;
RA Yoshida K., Seki S., Fujimura M., Miwa Y., Fujita Y.;
RT "Cloning and sequencing of a 36-kb region of the Bacillus subtilis
RT genome between the gnt and tol operons.";
RL DNA Res. 2:61-69(1995).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=168;

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RX MEDLINE=95311309; PubMed=7540694;
RA Gardan R., Rapoport G., Debarbouille M.;
RT "Expression of the rocDEF operon involved in arginine catabolism in
RL Bacillus subtilis.";
RJ J. Mol. Biol. 249:843-856(1995).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertoletti M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruchi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinou S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Toseato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzengger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RL subtilis.";
RJ Nature 390:249-256(1997).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; D78193; HAAL1297.1; -.
DR EMBL; Z99124; CAB16075.1; -.
KW Complete proteome.
SQ SEQUENCE 280 AA; 32594 MW; 991C958F7F58C77 CRC64;

Query Match 55.3%; Score 42; DB 16; Length 280;
Best Local Similarity 72.7%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTD 11
Db 152 YEGHYIQKTD 162

RESULT 14
Q9A5R9 PRELIMINARY; PRT; 324 AA.
AC Q9A5R9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NAD-dependent epimerase/dehydratase family protein.
GN CC2378.

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OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Eisen J., Heideberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vanathavan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RJ Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RL EMBL; AE005907; AK24349.1; -.
DR TIGR; CC2378; -.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
KW Complete proteome.
SQ SEQUENCE 324 AA; 35414 MW; A5CB1D612F01EBDF CRC64;

Query Match 55.3%; Score 42; DB 16; Length 324;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13
Db 244 GGHEVYNGDND 255

RESULT 15
Q8RCV8 PRELIMINARY; PRT; 326 AA.
AC Q8RCV8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Lipote-protein ligase A.
GN LPLA OR TTE0297.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RJ Genome Res. 12:689-700(2002).
RL EMBL; AE013002; AAM23593.1; -.
DR InterPro; IPR004143; BPL_LipA_LipB.
DR InterPro; IPR004562; Lipoyltrans.
DR Pfam; PF03099; BPL_LipA_LipB; 1.
DR TIGRFAMs; TIGR00545; lipoyltrans; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 326 AA; 37543 MW; 2363F8E2F981D944 CRC64;

Query Match 55.3%; Score 42; DB 16; Length 326;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13
Db 208 GGGEMVEFTED 219

Search completed: October 14, 2003, 08:40:16

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Tue Oct 14 10:50:38 2003

us-09-931-700-2.rspt

Page 8

Job time : 21.4318 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:34:01 ; Search time 52.1364 Seconds
(without alignments)
94.378 Million cell updates/sec

Title: US-09-931-700-3

Perfect score: 163

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	100.0	31	18	AAW25160 Human preproadreno
2	163	100.0	31	22	AAW25160 Adrenomedullin pep
3	163	100.0	31	22	AAE09827 Human adrenomedull
4	163	100.0	52	22	AAW75110 Human adrenomedull
5	163	100.0	52	22	AAW75110 Adrenomedullin pep
6	163	100.0	52	22	AAE09818 Human adrenomedull
7	163	100.0	52	24	ABP5104 Human adrenomedull
8	163	100.0	53	22	AAW75111 Glycine extended h
9	163	100.0	53	22	AAW75112 Glycine extended a

10	163	100.0	53	24	ABJ18665 Universal stress p
11	163	100.0	62	22	AAW75113 Linker peptide-adr
12	163	100.0	120	22	AAW75122 UsPA(1-57)-(A)-(GS
13	163	100.0	120	22	AAW75123 UsPA(1-56)-(DD)-(G
14	163	100.0	120	24	ABJ18669 Universal stress p
15	163	100.0	120	24	ABJ18670 Universal stress p
16	163	100.0	147	22	AAW75124 UsPA(1-84)-(A)-(GS
17	163	100.0	147	24	ABJ18671 Universal stress p
18	163	100.0	170	22	AAW75114 Thiorodoxin-(GSGSG
19	163	100.0	185	22	AAW49697 Human adrenomedull
20	163	100.0	185	22	AAW60344 Human adrenomedull
21	163	100.0	185	24	ABP72347 Adrenomedullin, in
22	163	100.0	206	24	ABJ18668 Adrenomedullin, in
23	157	96.3	188	22	AAW49698 Porcine adrenomedu
24	157	96.3	188	22	AAW60345 Porcine adrenomedu
25	148	90.8	40	22	AAW75178 Adrenomedullin pep
26	148	90.8	50	22	AAE09819 Rat adrenomedullin
27	148	90.8	185	22	AAW49699 Rat adrenomedullin
28	148	90.8	185	22	AAW60346 Rat adrenomedullin
29	140	85.9	184	23	ABW57209 Mouse ischaemic co
30	136.5	83.7	53	22	AAW75176 Adrenomedullin pep
31	123.5	77.0	37	22	AAW91761 Adrenomedullin pep
32	123.5	75.8	52	22	AAW91765 Adrenomedullin pep
33	57	35.0	13	18	AAW25159 Human preproadreno
34	52	31.9	229	22	ABG05415 Novel human diagno
35	52	31.9	229	22	ABG13273 Novel human diagno
36	52	31.9	677	22	ABW9129 Novel human diagno
37	52	31.9	775	19	AAW58582 Kojibiose phosphor
38	52	31.9	939	22	ABG14932 Novel human diagno
39	52	31.9	994	22	ABG10411 Novel human diagno
40	51.5	31.6	620	23	ABP66343 Bifidobacterium lo
41	51	31.3	10	15	AAW67024 Hypotensive peptid
42	51	31.3	892	22	ABW62270 Drosophila melanog
43	51	31.3	1096	22	ABG19648 Novel human diagno
44	50	30.7	436	19	AAW56306 Clas I S-locus gly
45	50	30.7	846	19	AAW56307 Clas I S-receptor

ALIGNMENTS

RESULT 1
AAW25160
ID AAW25160 standard; peptide; 31 AA.
AC AAW25160;
XX
XX AAW25160;
DT 08-DEC-1997 (first entry)
XX Human preproadrenomedullin derived immunogen, P072.
DE
DE Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone;
KW skin; blood related; disease; type II diabetes; preeclampsia;
KW neurotransmission regulation; allergy; mast cell degranulation;
KW antibacterial; antifungal; wound repair.
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..31
XX Modified-site 31 /note= "residues 116-146 of preproadrenomedullin"
XX FT /note= "amidated"

XX WO9707214-A1.
XX 27-FEB-1997.
XX
XX 16-AUG-1996; 96WO-US3286.
XX
XX 12-MAR-1996; 96US-0013172.
XX 18-AUG-1995; 95US-0002514.
XX 30-AUG-1995; 95US-0002936.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX
 PI Cuttitta F, Gray K, Hook W, Macri C, Martinez A;
 PI Miller MJ, Unsworth EJ, Walsh T;
 XX
 XX WPI; 1997-165298/15.
 XX
 XX Human adrenomedullin peptide(s), PO70, PO71, PO72 and PAMP-20 - used
 PT in the diagnosis and treatment of type II diabetes and cancer
 XX
 PS Claim 1; Page 43; 106pp; English.
 XX
 XX Human adrenomedullin (AM) peptides PO70, PO71, PO72 and PAMP-20
 CC were used for the production of anti-AM antibodies (Ab). PO70 represents
 CC preproAM amino acids (aa) 34-41 with the sequence Tyr-Tyr attached at
 CC the N-terminus, PO71 represents preproAM aa 122-131 with the sequence
 CC Tyr-Gly-Gly attached at the N-terminus, PO72 represents preproAM aa
 CC 116-146 and PAMP-20 represents the proAM N-terminus. The Ab are useful
 CC for the prevention and/or treatment of cancers, e.g. adrenal, nervous
 CC system, lung, colon, ovarian and breast cancer by inhibiting cell
 CC growth. They are also useful for regulating insulin secretion and blood
 CC glucose metabolism and therefore for treating and/or preventing diabetes
 CC type II. They may be used for the diagnosis or treatment of conditions
 CC relating to pregnancy e.g. preeclampsia. The Ab are also useful
 CC for the following: (i) regulating neurotransmission or neuron growth in
 CC areas of the central nervous system; (ii) lessening or inhibiting mast
 CC cell degranulation and hence reducing the effects of an allergic
 CC response; (iii) inhibiting or preventing bacterial and fungal growth (to
 CC treat infection); (iv) facilitating wound healing; and (v) promoting
 CC organ and bone development.
 XX
 SQ Sequence 31 AA;
 Query Match 100.0%; Score 163; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPOGY 31
 Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPOGY 31
 RESULT 2
 AAB91762
 ID AAB91762 standard; Peptide; 31 AA.
 XX
 AC AAB91762;
 DT 22-JUN-2001 (first entry)
 XX
 XX Adrenomedullin peptide (AM) SEQ ID NO:938.
 DE
 DE Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimide group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 OS
 OS Homo sapiens.
 OS Synthetic.
 XX WO200069900-A2.
 XX
 XX 23-NOV-2000.
 XX
 XX 17-MAY-2000; 2000WO-US13576.
 XX
 XX 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 XX (CONJ-) CONJUCHEM INC.
 PA Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 PI

XX WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 XX
 PS Disclosure; Page 499-500; 733pp; English.
 XX
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (IiI) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 31 AA;
 Query Match 100.0%; Score 163; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPOGY 31
 Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPOGY 31
 RESULT 3
 AAE09827
 ID AAE09827 standard; peptide; 31 AA.
 XX
 AC AAE09827;
 XX
 XX 29-NOV-2001 (first entry)
 DT
 DE Human adrenomedullin peptide #2.
 DE
 KW Human: vasoactive peptide; calcitonin gene related peptide; CGRP;
 KW CGRP-receptor identification; adrenomedullin.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 31
 FT /note= "C-terminal amide"
 XX
 XX US6268474-B1.
 PN
 XX 31-JUL-2001.
 XX
 XX 30-APR-1998; 98US-0070504.
 XX
 XX 30-APR-1998; 98US-0070504.
 PR
 XX (UYCR-) UNIV CREIGHTON.
 XX
 XX Smith DD, Saha S, Abel PW;
 XX
 XX WPI; 2001-564216/63.
 XX
 XX Vasoactive peptides useful for inhibiting calcitonin gene related
 PT peptide receptor activity -

XX PS Claim 5; Column 6; 24pp; English.

XX CC The invention relates to antagonists of the vasoactive peptide

CC CC calcitonin gene related peptide (CGRP) and other members of the

CC CC CGRP superfamily. The invention also relates to amino the terminal

CC CC modifications of peptides to improve their ability to bind to a

CC CC member of the CGRP-receptor super-family. CGRP antagonists are

CC CC used for inhibiting CGRP activity which can be used in vitro e.g.

CC CC in assays to identify and/or isolate CGRP receptors or with intact

CC CC cells either in vitro or in vivo to inhibit the effect of CGRP

CC CC binding to its receptor. The present sequence is human

CC CC adrenomedullin peptide.

XX XX Sequence 31 AA;

SQ Query Match 100.0%; Score 163; DB 22; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.9e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 31

Db 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 31

RESULT 4

AAB75110

ID AAB75110 standard; Protein; 52 AA.

XX AC AAB75110;

XX DT 31-JUL-2001 (first entry)

XX DE Human adrenomedullin (AM) protein.

XX KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;

XX KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.

OS Homo sapiens.

XX XX WO200127310-A1.

XX PD 19-APR-2001.

XX PF 10-OCT-2000; 2000WO-JP07023.

XX PR 15-OCT-1999; 99JP-0294147.

XX XX (SHIO) SHIONOGI & CO LTD.

XX PA Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;

XX PI WPI; 2001-282044/29.

XX DR N-PSDB; AAH19806.

XX PT Producing adrenomedullin useful for pharmaceutical and diagnostic

PT application comprises producing fused adrenomedullin precursor using a

PT recombinant host

XX PS Disclosure; Page 45; 75pp; Japanese.

XX CC The present invention describes a method (M1) for producing

CC CC adrenomedullin precursor. The method comprises: (a) producing the fused

CC CC protein using a recombinant host cell; (b) restricted digestion of the

CC CC fused protein by a protease followed by collection of sediment; and

CC CC (c) dissolving the sediment and extracting adrenomedullin precursor.

CC CC The method can be used for the production of adrenomedullin precursor

CC CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866

CC CC and AAB75110 to AAB75124 represent sequences which are used in the

XX XX exemplification of the present invention.

SQ Sequence 52 AA;

Query Match 100.0%; Score 163; DB 22; Length 52;

Best Local Similarity 100.0%; Pred. No. 3.6e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 31

Db 22 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 52

RESULT 5

AAB91759

ID AAB91759 standard; Peptide; 52 AA.

XX AC AAB91759;

XX DT 22-JUN-2001 (first entry)

XX DE Adrenomedullin peptide (AM) SEQ ID NO:935.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;

XX KW blood component; modification; succinimidy; maleimido group; amino;

XX KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS OS Synthetic.

XX PN WO2000069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure; Page 498; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)

CC CC comprising a therapeutically active amino acid region (III) and a

CC CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to

CC CC a less therapeutically active amino acid region (IV), which covalently

CC CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC CC peptidase stabilised therapeutic peptide composed of 3-30 amino acids.

CC CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC CC factors and neurotransmitters, to protect them from peptidase activity

CC CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC CC peptides are not suitable as drug candidates as they require frequent

CC CC administration due to rapid degradation by peptidases in the body.

CC CC Modifying and attaching therapeutic peptides to albumin prevents or

CC CC reduces the action of peptidases to increase length of activity (half

CC CC life) and specificity as bonding to large molecules decreases

CC CC intracellular uptake and interference with physiological processes.

CC CC AAB90829 to AAB92441 represent peptides which can be used in the

CC CC exemplification of the present invention.

XX SQ Sequence 52 AA;

Query Match 100.0%; Score 163; DB 22; Length 52;

Best Local Similarity 100.0%; Pred. No. 3.6e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 31

DR N-PSDB; AAH19865.

PT Producing adrenomedullin useful for pharmaceutical and diagnostic

PT application comprises producing fused adrenomedullin precursor using a

PT recombinant host

XX

PS Claim 17; Page 69-70; 75pp; Japanese.

XX

CC The present invention describes a method (M1) for producing

CC adrenomedullin precursor. The method comprises: (a) producing the fused

CC protein using a recombinant host cell; (b) restricted digestion of the

CC fused protein by a protease followed by collection of sediment; and

CC (c) dissolving the sediment and extracting adrenomedullin precursor.

CC The method can be used for the production of adrenomedullin precursor

CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866

CC and AAB75110 to AAB75124 represent sequences which are used in the

CC exemplification of the present invention.

XX

SQ Sequence 120 AA;

Query Match 100.0%; Score 163; DB 22; Length 120;

Best Local Similarity 100.0%; Pred. No. 9.9e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

DB 89 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 119

RESULT 14

ABJ18669

ID ABJ18669 standard; Protein; 120 AA.

AC ABJ18669;

XX

XX 27-FEB-2003 (first entry)

DE Universal stress protein A (uspa)-related protein #4.

XX

XX Fusion peptide; universal stress peptide; uspa; linker peptide;

KW large scale peptide production.

XX

OS Unidentified.

XX

XX WO200283907-A1.

PN

XX

PD 24-OCT-2002.

XX

PF 04-APR-2002; 2002WO-JP03374.

XX

PR 10-APR-2001; 2001JP-0111088.

XX

PA (SHIO) SHIONOGI & CO LTD.

XX

PI Mitsuda Y;

XX

XX WPI; 2003-067581/06.

DR

DR N-PSDB; ABT14529.

XX

PT Fusion polypeptide of Escherichia coli universal stress peptide with a

PT target peptide, useful for efficient large scale production of the

PT target peptide comprising expression of the fusion polypeptide followed

PT by cleavage

XX

PS Claim 5; Page 36; 49pp; Japanese.

XX

CC The invention comprises a novel fusion peptide which contains an

CC Escherichia coli universal stress protein (Usps), a linker peptide and a

CC target peptide. The fusion protein is cleavable by a protease. The fusion

CC peptide of the invention is useful for the efficient large scale

CC production of peptides. The present amino acid sequence represents a

XX protein that was used in the invention.

SQ Sequence 120 AA;

Query Match 100.0%; Score 163; DB 24; Length 120;

Best Local Similarity 100.0%; Pred. No. 9.9e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

DB 89 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 119

RESULT 15

ABJ18670

ID ABJ18670 standard; Protein; 120 AA.

XX

XX ABJ18670;

XX

XX 27-FEB-2003 (first entry)

DE Universal stress protein A (uspa)-related protein #5.

XX

XX Fusion peptide; universal stress peptide; uspa; linker peptide;

KW large scale peptide production.

XX

OS Unidentified.

XX

XX WO200283907-A1.

PN

XX

PD 24-OCT-2002.

XX

PF 04-APR-2002; 2002WO-JP03374.

XX

PR 10-APR-2001; 2001JP-0111088.

XX

PA (SHIO) SHIONOGI & CO LTD.

XX

PI Mitsuda Y;

XX

XX WPI; 2003-067581/06.

DR

DR N-PSDB; ABT14530.

XX

PT Fusion polypeptide of Escherichia coli universal stress peptide with a

PT target peptide, useful for efficient large scale production of the

PT target peptide comprising expression of the fusion polypeptide followed

PT by cleavage

XX

PS Claim 5; Page 38; 49pp; Japanese.

XX

CC The invention comprises a novel fusion peptide which contains an

CC Escherichia coli universal stress protein (Usps), a linker peptide and a

CC target peptide. The fusion protein is cleavable by a protease. The fusion

CC peptide of the invention is useful for the efficient large scale

CC production of peptides. The present amino acid sequence represents a

XX protein that was used in the invention.

SQ Sequence 120 AA;

Query Match 100.0%; Score 163; DB 24; Length 120;

Best Local Similarity 100.0%; Pred. No. 9.9e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

DB 89 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 119

Search completed: October 14, 2003, 08:38:47

Job time : 53.1364 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:36:56 ; Search time 17,6136 Seconds
(without alignments)
169.257 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	100.0	185	JN0684	adrenomedullin pre
2	157	96.3	188	S41500	adrenomedullin p
3	148	90.8	185	JN0766	adrenomedullin pre
4	58.5	35.9	189	A99638	hypothetical prote
5	58.5	35.9	189	A85489	hypothetical prote
6	58	35.6	430	T14536	S-locus-specific g
7	56	34.4	431	T14415	S-locus-specific g
8	54	33.1	373	G84107	lipopolysaccharide
9	53	32.5	465	T15540	hypothetical prote
10	52	31.9	428	T14529	S-locus-specific g
11	51	31.3	428	T07814	S-locus-specific g
12	51	31.3	429	T14533	S-locus-specific g
13	51	31.3	436	A27827	S-locus-specific g
14	51	31.3	857	T14471	probable S-recepto
15	50	30.7	90	C86279	hypothetical prote
16	50	30.7	427	T14424	S-locus-specific g
17	50	30.7	428	T14423	S-locus-specific g
18	49	30.1	428	T14416	S-locus-specific g
19	49	30.1	428	T14530	S-locus-specific g
20	49	30.1	429	T07809	S-receptor kinase
21	49	30.1	429	T14528	S-locus-specific g
22	49	30.1	431	T07812	S-locus-specific g
23	49	30.1	431	T14418	S-locus-specific g
24	49	30.1	434	S04906	S-locus-specific g
25	48.5	29.8	322	T47067	hypothetical prote
26	48	29.4	328	AG0363	probable cell divi
27	48	29.4	416	TJ1343	glycopeptide N-te
28	48	29.4	426	T07810	S-locus-specific g
29	48	29.4	444	E69130	histidine-trNA lig

ALIGNMENTS

RESULT 1

JN0684
adrenomedullin precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C:Accession: JC2351; JN0684; P0548; JN0476
R:ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuo, K.; Eto, T.
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A:Title: Genomic structure of human adrenomedullin gene.
A:Reference number: JC2351; MUID:94354869; PMID:8074714
A:Accession: JC2351
A:Molecule type: DNA
A:Residues: 1-185 <ISH>
A:Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
A:Experimental source: pheochromocytoma
R:Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A:Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
A:Reference number: JN0684; MUID:93343928; PMID:7688224
A:Accession: JN0684
A:Molecule type: mRNA
A:Residues: 1-185 <KIT>
A:Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A:Accession: P0548
A:Molecule type: protein
A:Residues: 22-41 <KIT>
R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A:Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A:Reference number: JN0476; MUID:93249425; PMID:8367282
A:Accession: JN0476
A:Molecule type: protein
A:Residues: 95-146 <KIT>
A:Experimental source: pheochromocytoma
C:Genetics:
A:Gene: GDB:ADM
A:Cross-references: GDB:217070; OMIM:103275
A:Map position: 1pter-1lqter
C:Keywords: amidated carboxyl end; blood pressure control; hormone
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-185/Product: proadrenomedullin #status predicted <PEU>
F:22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F:95-146/Product: adrenomedullin #status experimental <NAR>
F:147-185/Domain: carboxyl-terminal propeptide #status predicted <CPT>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F:110-115/bisulfide bonds: #status experimental
F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match 100.0%; Score 163; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.3e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
 |||||
 Db 116 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 146

RESULT 2
 S41600
 adrenomedullin - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C:Accession: S41600
 R:Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
 FEBS Lett. 338, 306-310, 1994
 A>Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encoding
 A:Reference number: S41600; MUID:94139945; PMID:8043068
 A:Accession: S41600
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-188 <KIT>
 A:Cross-references: GB:D14875; NID:9439721; PIDN:BAA03590.1; PID:9496379

Query Match 96.3%; Score 157; DB 2; Length 188;
 Best Local Similarity 96.8%; Pred. No. 1.8e-15;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
 |||||
 Db 116 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 146

RESULT 3
 JN0766
 adrenomedullin precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
 C:Accession: JN0766; P0610
 R:Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T.
 Biochem. Biophys. Res. Commun. 195, 921-927, 1993
 A>Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensive
 A:Reference number: JN0766; MUID:93384621; PMID:7690563
 A:Accession: JN0766
 A:Molecule type: mRNA
 A:Residues: 1-185 <SAK>
 A:Accession: P0610
 A:Molecule type: protein
 A:Residues: 22-41 <SAZ>
 C:Comment: This precursor contains a unique 20-amino acid sequence designated proadrenomedullin
 C:Keywords: amidated carboxyl end
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-185/Product: proadrenomedullin #status predicted <PEU>
 F:22-41/Product: proadrenomedullin amino-terminal 20 peptide
 F:94-143/Product: adrenomedullin #status predicted <MAT>
 F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
 F:143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 90.8%; Score 148; DB 2; Length 185;
 Best Local Similarity 87.1%; Pred. No. 3.7e-14;
 Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
 |||||
 Db 113 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 143

RESULT 4
 A99638
 hypothetical protein EC0073 [imported] - Escherichia coli (strain O157:H7, substrain R1
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C:Accession: A99638
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: A99638
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-189 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA033496.1; PID:gl3359529; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain R1MD 0509952
 C:Genetics:
 A:Gene: EC0073
 C:Superfamily: Escherichia coli yabp protein

Query Match 35.9%; Score 58.5; DB 2; Length 189;
 Best Local Similarity 34.4%; Pred. No. 0.5;
 Matches 11; Conservative 9; Mismatches 7; Indels 5; Gaps 1;

QY 4 KLAHQIYQFTD-----KDKDNVAPRSKISPG 30
 ||| : : : || : : : || : : : || :
 Db 95 KLTHWLKFNELKEYAKDPENNAKASLSPEG 126

RESULT 5
 A85489
 hypothetical protein 20078 [imported] - Escherichia coli (strain O157:H7, substrain E
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: A85489
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
 Nature 409, 529-533, 2001
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85489; MUID:21074935; PMID:11206551
 A:Accession: A85489
 A:Molecule type: DNA
 A>Status: preliminary
 A:Residues: 1-189 <STO>
 A:Cross-references: GB:AE005174; NID:gt12512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP:
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: 20078
 C:Superfamily: Escherichia coli yabp protein

Query Match 35.9%; Score 58.5; DB 2; Length 189;
 Best Local Similarity 34.4%; Pred. No. 0.5;
 Matches 11; Conservative 9; Mismatches 7; Indels 5; Gaps 1;

QY 4 KLAHQIYQFTD-----KDKDNVAPRSKISPG 30
 ||| : : : || : : : || : : : || :
 Db 95 KLTHWLKFNELKEYAKDPENNAKASLSPEG 126

RESULT 6
 T14536
 S-locus-specific glycoprotein - wild cabbage (fragment)
 N:Alternate names: S glycoprotein
 C:Species: Brassica oleracea (wild cabbage)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
 C:Accession: T14536
 R:Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
 Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
 A>Title: Striking sequence similarity in inter- and intra-specific comparisons of cl
 mechanism.
 A:Reference number: Z18078; MUID:97352858; PMID:9207151
 A:Accession: T14536
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-430 <KUS>
 A:Cross-references: EMBL:D85212; NID:g2351155; PIDN:BAA21946.1; PID:g2351156
 C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
 C:Keywords: glycoprotein

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of *C. elegans* cosmid C17C3.

A:Reference number: Z18366

A:Accession: T15540

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-465 <DUZ>

A:Cross-references: EMBL:U41279; NID:g1086905; PID:g1086919; PIDN:AAB52685.1; GSPDB:G

A:Experimental source: strain Bristol N2; clone C17C3

C:Genetics:

A:Gene: CESP:C17C3.1

A:Map position: 2

A:Introns: 124/2; 138/2; 174/2; 223/1; 369/2

Query Match 32.5%; Score 53; DB 2; Length 465;

Best Local Similarity 40.0%; Pred. No. 8.7;

Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 OKLAHOLYQFTDKDNVAP 22
|::||:::|::|::|::|

Db 156 QETAHKFFDFTLKKDSFSP 175
|::||:::|::|::|::|

RESULT 10

T14529

S-locus-specific glycoprotein - wild cabbage (fragment)

N:Alternate names: S glycoprotein

C:Species: Brassica oleracea (wild cabbage)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000

C:Accession: T14529

R:Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.

A:Title: Striking sequence similarity in inter- and intra-specific comparisons of a cl

A:Reference number: Z18078; MUID:97352858; PMID:9207151

A:Accession: T14529

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-428 <KUS>

A:Cross-references: EMBL:D85205; NID:g2351141; PIDN:BAA21939.1; PID:g2351142

C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology

C:Keywords: glycoprotein

Query Match 31.9%; Score 52; DB 2; Length 428;

Best Local Similarity 28.2%; Pred. No. 11;

Matches 11; Conservative 8; Mismatches 10; Indels 10; Gaps 1;

QY 3 OKLAHOLYQFTDKDKD-----NVAPRSKISPGY 31
|::||:::|::|::|::|

Db 229 QKLSIMVINTENSEVAYTFRTNNFSYRLKVSDDGY 267
|::||:::|::|::|::|

RESULT 11

T07814

S-locus-specific glycoprotein S6 - radish (fragment)

C:Species: Raphanus sativus (radish)

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000

C:Accession: T07814

R:Sakamoto, K.; Kusaba, M.; Nishio, T.

Mol. Gen. Genet. 258, 397-403, 1998

A:Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus related

A:Reference number: Z16146; MUID:98311079; PMID:9648745

A:Accession: T07814

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-428 <SAK>

A:Cross-references: EMBL:AB009682; NID:g3327849; PIDN:BAA31729.1; PID:g3327850

C:Genetics:

A:Gene: SLG(S6)

C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology

C:Keywords: glycoprotein

F:32-426/Domain: S-locus-specific glycoprotein homology <SSG>

Query Match 31.3%; Score 51; DB 2; Length 428;
Best Local Similarity 28.2%; Pred. No. 16;
Matches 11; Conservative 8; Mismatches 10; Indels 10; Gaps 1;

QY 3 QKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
||||: :| | : : : :| | | |
Db 229 QKLSYVYNFTENSEEVAYFTLMTNNSIYSLTISSEGY 267

RESULT 12
T14533
S-locus-specific glycoprotein - wild cabbage (fragment)
N:Alternate names: S glycoprotein
C:Species: Brassica oleracea (wild cabbage)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C:Accession: T14533
R:Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A:Title: Striking sequence similarity in inter- and intra-specific comparisons of a class
echanism.
A:Reference number: Z18078; MUID:97352858; PMID:9207151
A:Accession: T14533
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-429 <KUS>
A:Cross-references: EMBL:D85209; NID:92351149; PIDN:BAA21943.1; PID:92351150
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein

Query Match 31.3%; Score 51; DB 2; Length 429;
Best Local Similarity 32.5%; Pred. No. 16;
Matches 13; Conservative 8; Mismatches 7; Indels 12; Gaps 2;

QY 3 QKLAHQIYQFTDKDKDVA-----PRSKISPGY 31
||||: :| | : :| | : :| | :
Db 230 QKLSYVYNFTEDSEEVAYFTMTNNSIYSLTISSEGF 268

RESULT 13
A27827
S-locus-specific glycoprotein S6 precursor - wild cabbage
C:Species: Brassica oleracea (wild cabbage)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 15-Nov-1996
C:Accession: A27827
R:Nasrallah, J.B.; Kao, T.H.; Chen, C.H.; Goldberg, M.L.; Nasrallah, M.E.
Nature 326, 617-619, 1987
A:Title: Amino-acid sequence of glycoproteins encoded by three alleles of the S locus of
A:Reference number: A93392
A:Accession: A27827
A:Molecule type: mRNA
A:Residues: 1-436 <NAS>
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-436/Product: S-locus-specific glycoprotein S6 #status predicted <MAT>
F:40-434/Domain: S-locus-specific glycoprotein homology <SSG>

Query Match 31.3%; Score 51; DB 2; Length 436;
Best Local Similarity 25.6%; Pred. No. 16;
Matches 10; Conservative 10; Mismatches 9; Indels 10; Gaps 1;

QY 3 QKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
||||: :| | : : : :| | | |
Db 237 QKLSYVYNFTENSEEVAYFTMTNNSIYSLTISSEGY 275

RESULT 14
T14471
probable S-receptor kinase (EC 2.7.1.-) srk29 - wild cabbage
C:Species: Brassica oleracea (wild cabbage)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T14471
R:Kumar, V.; Trick, M.

Plant J. 6, 807-813, 1994
A:Title: Expression of the S-locus receptor kinase multigene family in Brassica olera
A:Reference number: Z18108; MUID:95152555; PMID:7849734
A:Accession: T14471
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-857 <KUM>
A:Cross-references: EMBL:Z30211; NID:9459244; PIDN:CAA82930.1; PID:9459245
A:Experimental source: strain alboglabra; stigma
C:Genetics:
A:Gene: srk29
A:Introns: 438/1; 481/1; 544/3; 615/1; 694/2; 744/3
C:Function:
A:Description: Implicated in the self-incompatibility system of Brassica oleracea
C:Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot
C:Keywords: Anp; phosphotransferase; serine/threonine-specific protein kinase; signal
F:41-436/Domain: S-locus-specific glycoprotein homology <SSG>
F:536-813/Domain: protein kinase homology <KIN>

Query Match 31.3%; Score 51; DB 2; Length 857;
Best Local Similarity 28.2%; Pred. No. 34;
Matches 11; Conservative 8; Mismatches 10; Indels 10; Gaps 1;

QY 3 QKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
||||: :| | : :| | : :| | :
Db 239 QKLSYVYNFTQNSEVYVFTMTNNSIYSLTISSEGY 277

RESULT 15

C86279
hypothetical protein F14L17.23 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: C86279
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
ansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86279
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STO>
A:Cross-references: GB:AE005172; NID:97262688; PIDN:AAF43946.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 30.7%; Score 50; DB 2; Length 90;
Best Local Similarity 41.9%; Pred. No. 3.8;
Matches 13; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
||||: :| | : :| | : :| | :
Db 12 TVQTIARPTDEDKIQTVPPPSKHTPPGY 42

Search completed: October 14, 2003, 08:40:50
Job time : 19.6136 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:35:36 ; Search time 9.86364 Seconds
(without alignments)
147.798 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	100.0	185	1	ADML_HUMAN
2	157	96.3	188	1	ADML_PIG
3	152	93.3	188	1	ADML_CANFA
4	148	90.8	185	1	ADML_RAT
5	146	89.6	188	1	ADML_BOVIN
6	140	85.9	184	1	ADML_MOUSE
7	51.5	31.6	620	1	ILVD_BIFLO
8	51	31.3	436	1	SLS6_BRAOL
9	49	30.1	180	1	VG48_BPMU
10	49	30.1	435	1	SLS2_BRAOA
11	48.5	29.8	322	1	Y4KA_RHLSN
12	48	29.4	328	1	ZIPA_YERPE
13	48	29.4	425	1	SYH_METH
14	48	29.4	496	1	NMT1_HUMAN
15	48	29.4	496	1	NMT1_MOUSE
16	48	29.4	497	1	NMT1_BOVIN
17	48	29.4	689	1	UVRA_PSELE
18	47.5	29.1	438	1	PRIL_DROME
19	47	28.8	545	1	FLIF_BUCAL
20	47	28.8	1268	1	VGLN_HUMAN
21	47	28.8	1541	1	MRP2_RAT
22	46.5	28.5	339	1	LPXD_YEREN
23	46.5	28.5	941	1	DNAB_RHOMR
24	46	28.2	434	1	SLS3_BRAOL
25	46	28.2	441	1	SPAC_BACSU
26	46	28.2	453	1	GATA_CAME
27	46	28.2	461	1	MIG6_MOUSE
28	46	28.2	922	1	YKFO_YEAST
29	46	28.2	1545	1	MRP2_HUMAN
30	46	28.2	4447	1	PKSK_BACSU
31	45	27.6	235	1	HG12_CAEEL
32	45	27.6	459	1	MIG6_RAT
33	45	27.6	576	1	SYPC_YEAST

34	45	27.6	599	1	FRDA_HAEIN
35	45	27.6	845	1	CC47_YEAST
36	45	27.6	2245	1	MYSU_DICDI
37	45	27.6	2493	1	YBA4_YEAST
38	45	27.6	2778	1	FAF_DROME
39	45	27.6	3511	1	MY15_MOUSE
40	45	27.6	3530	1	MY15_HUMAN
41	44.5	27.3	136	1	GCS3_SUITO
42	44.5	27.3	426	1	YK96_AERPE
43	44.5	27.3	520	1	LAC1_AGABI
44	44.5	27.3	520	1	LAC2_AGABI
45	44.5	27.3	703	1	COAT_SMSV4

ALIGNMENTS

RESULT 1

ID	ADML_HUMAN	STANDARD	PRT	185 AA
AC	P35318			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)).			
GN	ADM OR AM			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pheochromocytoma;			
RX	MEDLINE=93343928; PubMed=7686224;			
RA	Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;			
RT	"Cloning and characterization of cDNA encoding a precursor for human adrenomedullin."			
RL	Biochem. Biophys. Res. Commun. 194:720-725(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=94354869; PubMed=8074714;			
RA	Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,			
RT	Kitamura K., Eto T., Matsuo H.;			
RL	"Genomic structure of human adrenomedullin gene."			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
[4]				
RP	SEQUENCE OF 95-146.			

P44894 haemophilus
P38132 saccharomyc
P54697 dictyostell
P35194 saccharomyc
P55824 drosophila
Q9qz24 mus musculu
Q9ukn7 homo sapien
Q96z07 sulfolobus
Q9ya42 aeropyrum p
Q12541 agaricus bi
Q12542 agaricus bi
P36285 san mignuel

RC TISSUE-Pheochromocytoma;
 RX MEDLINE=93249425; PubMed=8387282;
 RA Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
 RA Matsuo H., Eto T.;
 RT "Adrenomedullin: a novel hypotensive peptide isolated from human
 RT pheochromocytoma.";
 RL Biochem. Biophys. Res. Commun. 192:553-560(1993).
 RN [5]
 RN REVIEW.
 RP RX MEDLINE=98240137; PubMed=9578982;
 RA Samson W.K.;
 RT "Proadrenomedullin-derived peptides.";
 RL Front. Neuroendocrinol. 19:100-127(1998).
 RN [6]
 RN REVIEW.
 RP RX MEDLINE=20053666; PubMed=10588445;
 RA Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
 RT "Structure-activity relationships of adrenomedullin in the circulation
 RT and adrenal gland.";
 RL Regul. Pept. 85:1-8(1999).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE
 CC PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE
 CC KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP
 CC INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
 CC PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES
 CC INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN
 CC AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME,
 CC ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
 CC VESSELS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
 CC ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
 CC TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D14874; BAA03589.1; -;
 CC EMBL; S73906; AAC60642.1; -;
 CC EMBL; BC015961; AAH15961.1; -;
 CC EMBL; D43639; BAA07756.1; ALT_SEQ.
 CC PIR; JC2351; JN0684.
 CC Genew; HGNC:259; ADM.
 CC MTM; 103275; -;
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0006171; P:cAMP biosynthesis; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0008015; P:circulation; TAS.
 CC GO; GO:0007565; P:pregnancy; TAS.
 CC GO; GO:0006701; P:progesterone biosynthesis; TAS.
 CC GO; GO:0009611; P:response to wounding; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR001710; Adrenomedullin.
 CC Pfam; PF02039; Adrenomedullin; 1.
 CC PRINTS; PR00801; ADRENOMEDULLIN.
 CC Hormone; Amidation; Cleavage on pair of basic residues; Signal;
 CC Polymorphism.
 CC SIGNAL 1 21 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 CC PEPTIDE 22 41
 CC PROPEP 45 92
 CC PEPTIDE 95 146 ADRENOMEDULLIN.
 CC PROPEP 148 185 PREPROAM C-TERMINAL FRAGMENT.
 CC PEPTIDE 110 115
 CC DISULFID 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP).
 CC MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP).
 CC FT

FT VARIANT 50 50 S -> R (in dbSNP:5005).
 FT /FTid=VAR_014861.
 SQ SEQUENCE 185 AA; 20420 MW; 64C7D2A0B4654DFE CRC64;
 Query Match 100.0%; Score 163; DB 1; Length 185;
 Best local Similarity 100.0%; Pred. No. 4.2e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 31
 Db 116 TVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 146
 RESULT 2
 ADML_PIG STANDARD; PRT; 188 AA.
 ID ADML_PIG
 AC P33366;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM OR AM.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Adrenal medulla;
 RX MEDLINE=94139945; PubMed=8043068;
 RA Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
 RT "Complete amino acid sequence of porcine adrenomedullin and cloning
 RT of cDNA encoding its precursor.";
 RL FEBS Lett. 338:306-310(1994).
 RN [2]
 RN SEQUENCE OF 22-41.
 RC TISSUE-Adrenal medulla;
 RX MEDLINE=94357274; PubMed=8076689;
 RA Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
 RA Kawamoto M., Minamino N., Matsuo H., Eto T.;
 RT "Identification and hypotensive activity of proadrenomedullin
 RT N-terminal 20 peptide (PAMP).";
 RL FEBS Lett. 351:35-37(1994).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
 CC KIDNEY
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; D14875; BAA03590.1; -;
 CC PIR; S41600; S41600.
 CC InterPro; IPR001710; Adrenomedullin.
 CC Pfam; PF02039; Adrenomedullin; 1.
 CC PRINTS; PR00801; ADRENOMEDULLIN.
 CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 CC SIGNAL 1 21
 CC PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 CC PROPEP 45 92
 CC PEPTIDE 95 146 ADRENOMEDULLIN.
 CC PROPEP 153 188 PREPROAM C-TERMINAL FRAGMENT (BY
 CC SIMILARITY).
 CC DISULFID 110 115 BY SIMILARITY.
 CC MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP).
 CC FT

FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 188 AA; 20893 MW; 71749460F5660A61 CRC64;

Query Match
 Best Local Similarity 96.3%; Score 157; DB 1; Length 188;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31
 |||||
 Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 3
 ADML_CANFA
 ID ADML_CANFA STANDARD; PRT; 188 AA.
 AC 077559; Q9TVC9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Imoto I., Jougasaki M.;
 RT "Cloning of cDNA encoding canine adrenomedullin.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99002704; PubMed=9788655;
 RX Ono Y., Kojima M., Okada K., Kangawa K.;
 RA "cDNA cloning of canine adrenomedullin and its gene expression in the
 RT heart and blood vessels in endotoxin shock.";
 RL Shock 10:243-247(1998).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
 CC
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 CC
 CC EMBL; AF045773; AAD05423.1; -;
 CC EMBL; U96127; RAD09957.1; -;
 CC InterPro; IPR001710; Adrenomedullin.
 CC Pfam; PF02039; Adrenomedullin; 1.
 CC PRINTS; PR00801; ADRENOMEDULLIN.
 CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 CC SIGNAL 1 21 BY SIMILARITY.
 CC PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 CC FT PEPTIDE 22 41 BY SIMILARITY.
 CC FT PROPEP 45 92 BY SIMILARITY.
 CC FT PEPTIDE 95 146 ADRENOMEDULLIN.
 CC FT PROPEP 148 188 PREPROAM C-TERMINAL FRAGMENT (BY
 CC SIMILARITY).
 CC FT DISULFID 110 115 BY SIMILARITY.
 CC FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 CC (BY SIMILARITY).
 CC FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP)
 CC (BY SIMILARITY).
 CC FT CONFLICT 130 130 N -> K (IN REF. 2).
 CC FT SEQUENCE 188 AA; 20929 MW; 809D6A64F98F5578 CRC64;
 CC
 CC Query Match
 CC Best Local Similarity 93.3%; Score 152; DB 1; Length 188;
 CC Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31
 |||||
 Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 4
 ADML_RAT
 ID ADML_RAT STANDARD; PRT; 185 AA.
 AC P43145;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
 RX MEDLINE=93384621; PubMed=7690563;
 RA Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
 RA Matsuo H., Eto T.;
 RT "Molecular cloning and biological activities of rat adrenomedullin, a
 RT hypotensive peptide.";
 RL Biochem. Biophys. Res. Commun. 195:921-927(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=96102137; PubMed=8524787;
 RA Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
 RA Sulzpicio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
 RT "Discovery of adrenomedullin in rat ischemic cortex and evidence for
 RT its role in exacerbating focal brain ischemic damage.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY,
 CC HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
 CC
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 CC
 CC EMBL; D15069; BAA03665.1; -;
 CC EMBL; U15419; AAB60519.1; -;
 CC InterPro; IPR001710; Adrenomedullin.
 CC Pfam; PF02039; Adrenomedullin; 1.
 CC PRINTS; PR00801; ADRENOMEDULLIN.
 CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 CC SIGNAL 1 21 BY SIMILARITY.
 CC PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 CC FT PEPTIDE 22 41 BY SIMILARITY.
 CC FT PROPEP 45 91 BY SIMILARITY.
 CC FT PEPTIDE 94 143 ADRENOMEDULLIN.
 CC FT PROPEP 149 185 PREPROAM C-TERMINAL FRAGMENT (BY
 CC SIMILARITY).
 CC FT DISULFID 107 112 BY SIMILARITY.
 CC FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 CC (BY SIMILARITY).
 CC FT MOD_RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP)
 CC (BY SIMILARITY).
 CC FT SEQUENCE 185 AA; 20636 MW; 35CAD9A9DD19AE35 CRC64;

Query Match 90.8%; Score 148; DB 1; Length 185;
 Best Local Similarity 87.1%; Pred. No. 5.7e-14;
 Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 TVOKLAHQIYQFTDKDNVAPRSKISPOGY 31
 :|||||:|||||:|||||:|||||:|||||
 DB 113 TVOKLAHQIYQFTDKDNVAPRSKISPOGY 143

RESULT 5

ADML_BOVIN
 ID ADML_BOVIN STANDARD; PRT; 188 AA.
 AC 062827;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RX MEDLINE=98244567; PubMed=9581568;
 RA Barker S., Wood E., Clark A.J.L., Corder R.;
 RA "Cloning of bovine proadrenomedullin and inhibition of its basal
 RT expression in vascular endothelial cells by staurosporine.";
 RL Life Sci. 62:1407-1415(1998)
 CC -1- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
 CC CIRCULATION CONTROL (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.

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 CC -----

EMBL: AJ001613; CRA04866.1;
 DR InterPro: IPR001710; Adrenomedullin.
 DR Pfam: PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; ADRENOMEDULLIN.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PROPEP 45 92 BY SIMILARITY.
 FT PEPTIDE 95 146 ADRENOMEDULLIN.
 FT PROPEP 148 188 PREPROAM C-TERMINAL FRAGMENT (BY
 FT SIMILARITY).
 FT DISULFID 110 115 BY SIMILARITY.
 FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 SQ SEQUENCE 188 AA; 20981 MW; 3002E79AB3B6612C CRC64;

Query Match 89.6%; Score 146; DB 1; Length 188;
 Best Local Similarity 90.3%; Pred. No. 1.1e-13;
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TVOKLAHQIYQFTDKDNVAPRSKISPOGY 31
 :|||||:|||||:|||||:|||||:|||||
 DB 116 TVOKLAHQIYHFTDKDNVAPRSKISPOGY 146

RESULT 6

ADML_MOUSE
 ID ADML_MOUSE STANDARD; PRT; 184 AA.
 AC P97297; P97453;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=97092892; PubMed=8938454;
 RA Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
 RA Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
 RA "Genomic organization, expression, and chromosomal mapping of the
 RT mouse adrenomedullin gene.";
 RL Genomics 37:395-399(1996).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=C57BL/6J;
 CC MEDLINE=99046755; PubMed=9808778;
 CC Yotsumoto S., Shimada T., Cui C.Y., Nakashima H., Fujiwara H.,
 CC Ko M.S.H.;
 CC "Expression of adrenomedullin, a hypotensive peptide, in the
 CC trophoblast giant cells at the embryo implantation site in mouse.";
 CC Dev. Biol. 203:264-275(1998).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.

 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.

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EMBL: D78349; BAA11367.1;
 DR EMBL; U77630; AAB36535.1;
 DR MGD; MGI:108058; Adm.
 DR InterPro: IPR001710; Adrenomedullin.
 DR Pfam: PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; ADRENOMEDULLIN.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PROPEP 45 92 BY SIMILARITY.
 FT PEPTIDE 95 144 ADRENOMEDULLIN.
 FT PROPEP 151 184 PREPROAM C-TERMINAL FRAGMENT (BY
 FT SIMILARITY).
 FT DISULFID 108 113 BY SIMILARITY.
 FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT MOD_RES 144 144 AMIDATION (G-145 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT CONFLICT 173 173 A -> G (IN REF. 2).
 FT SEQUENCE 184 AA; 20764 MW; C88C99045A79C898 CRC64;

Query Match 85.9%; Score 140; DB 1; Length 184;
 Best Local Similarity 83.9%; Pred. No. 7.9e-13;
 Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 TVOKLAHQIYQFTDKDNVAPRSKISPOGY 31
 :|||||:|||||:|||||:|||||:|||||
 DB 114 TVOKLAHQIYQFTDKDNVAPRSKISPOGY 144


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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell division protein zipA homolog.
DE ZIPA OR IP02990 OR I1491.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Packhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Varra A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.B.;
RT "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 184:4601-4611(2002).
CC -1- FUNCTION: Interacts directly with the cell division proteinftsZ.
CC Probable receptor for the septal ring structure, may anchor it
CC to the inner-membrane (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (By
CC similarity).
CC -1- SIMILARITY: Belongs to the zipA family.
CC -----
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CC -----
DR EMBL; AJ141154; CAC92234.1; -
DR EMBL; AE013752; AM85062.1; ALT_INIT.
DR PIR; AG0363; AG0363.
DR HAMAP; MF_00509; -.
DR Pfam; PF04354; ZipA_C; 1.
DR Cell division; Septation; Transmembrane; Inner membrane;
DR KW Complete proteome.
DR DOMAIN 1 4 PERIPLASMIC (POTENTIAL).
DR TRANSMEM 5 25 POTENTIAL.
DR DOMAIN 26 328 CYTOPLASMIC (POTENTIAL).
DR SSQUENCE 328 AA; 36098 MW; EA04B89084649044 CRC64;
Query Match 29.4%; Score 48; DB 1; Length 328;
Best Local Similarity 36.7%; Pred. No. 19;
Matches 11; Conservative 6; Mismatches 11; Indels 2; Gaps 1;
QY 2 VOKLAHQI--YQFTDKDKDNVAPRSKISQ 29
Db 156 VERPAHQVAPQHQVESQEPVAPAPAKFQ 185
RESULT 13
SYN_METHTH STANDARD; PRT; 425 AA.
AC 026346;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
DE (HISRS).
DE HISS OR MTH244.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucet-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Adrege T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) -> AMP +
CC diphosphate + L-histidyl-tRNA(His).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC -----
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CC -----
DR EMBL; AE000811; AAB84750.1; ALT_INIT.
DR HSSP; O32422; LOF0.
DR HAMAP; MF_00127; 1.
DR InterPro; IPR004154; HGTP_anticonodon.
DR InterPro; IPR004516; Hiss.
DR InterPro; IPR002314; tRNA-synt_2b.
DR InterPro; IPR006195; tRNA_ligase_II.
DR Pfam; PF03129; HGTP_anticonodon.
DR Pfam; PF00587; tRNA-synt_2b; 1.
DR TIGRFAMS; TIGR00442; hiss; 1.
DR PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
DR KW Complete proteome.
DR SSQUENCE 425 AA; 48019 MW; 8388A5975A017535 CRC64;
Query Match 29.4%; Score 48; DB 1; Length 425;
Best Local Similarity 36.0%; Pred. No. 25;
Matches 9; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
QY 3 OKLAHQIYQFTDKDKDNVAPRSKIS 27
Db 56 EVVNVQIHFDTKGGRELALRSLT 80
RESULT 14
NMTH_HUMAN STANDARD; PRT; 496 AA.
AC P30419;
DT 01-APR-1993 (Rel. 25, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (peptide N-
DE myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase
DE 1) (NMT 1) (type 1 N-myristoyltransferase).
GN NMTH1 OR NMT.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE OF 58-496 FROM N.A., AND MUTAGENESIS OF GLY-492.
 RX MEDLINE=92237320; PubMed=1570339;
 RA Duronio R.J., Reed S.I., Gordon J.I.;
 RA "Mutations of human myristoyl-CoA:protein N-myristoyltransferase
 RT cause temperature-sensitive myristic acid auxotrophy in *Saccharomyces*
 RT *cerevisiae*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4129-4133(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98019247; PubMed=9353336;
 RA Glover C.J., Hartman K.D., Felsted R.L.;
 RA "Human N-myristoyltransferase amino-terminal domain involved in
 RT targeting the enzyme to the ribosomal subcellular fraction.";
 RL J. Biol. Chem. 272:28680-28689(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=98175914; PubMed=9506952;
 RA Giang D.K., Cravatt B.F.;
 RA "A second mammalian N-myristoyltransferase.";
 RT J. Biol. Chem. 273:6595-6598(1998).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RC TISSUE=Muscle, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.K., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN SEQUENCE OF 81-89 FROM N.A.
 RX MEDLINE=98343933; PubMed=9677304;
 RA McIlhinney R.A.J., Young K., Egerton M., Camble R., White A.,
 RA Soloviev M.;
 RA "Characterization of human and rat brain myristoyl-CoA:protein
 RT N-myristoyltransferase: evidence for an alternative splice variant of
 RT the enzyme.";
 RL Biochem. J. 333:491-495(1998).
 CC -!- FUNCTION: Adds a myristoyl group to the N-terminal glycine residue
 CC of certain cellular and viral proteins.
 CC -!- CATALYTIC ACTIVITY: Tetradecanoyl-CoA + glycyl-peptide = CoA + N-
 CC tetradecanoylglycyl-peptide.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P30419-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P30419-2; Sequence=VSP_003570;
 CC -!- TISSUE SPECIFICITY: HEART, GUT, KIDNEY, LIVER, AND PLACENTA.
 CC -!- SIMILARITY: BELONGS TO THE NMT FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC -----
 DR EMBL: M86707; -; NOT ANNOTATED_CDS.
 DR EMBL: AF043324; AAC03294.1; ALT_INIT.
 DR EMBL: AF020500; AAB95316.1; -
 DR EMBL: BC006538; AAH06538.1; -
 DR EMBL: BC006569; AAH06569.1; -
 DR EMBL: BC007258; AAH07258.1; -
 DR EMBL: BC008312; AAH08312.1; -
 DR EMBL: Y17209; CAH76686.1; -
 DR FIR: JCI343; JCI343.
 DR HSSP: P30418; INMT.
 DR Genew: HGNC:7857; NMT1.
 DR MIM: 160993; -
 DR GO: GO:0009249; P:protein-lipoylation; TAS.
 DR InterPro: IPR000903; Nmt.
 DR Pfam: PF01233; NMT_1.
 DR Pfam: PF02799; NMT_C; 1.
 DR PROSITE: PS00975; NMT_1; 1.
 DR PROSITE: PS00976; NMT_2; 1.
 KW Transferase; Acyltransferase; Alternative splicing.
 FT DOMAIN 55 67
 FT VARSPLIC 1 80
 FT MISSING (in isoform Short).
 FT MUTAGEN 492 492 /FTID=VSP_003570.
 FT G->D,K: REDUCED ACTIVITY.
 SQ SEQUENCE 496 AA; 56806 MW; 7661140D3837BE7A CRC64;
 Query Match 29.4%; Score 48; DB 1; Length 496;
 Best Local Similarity 24.5%; Pred. No. 29;
 Matches 12; Conservative 7; Mismatches 12; Indels 18; Gaps 1;
 QY 1 TVQKLAHQIYQFTD-----KDKDNVAPRSKISPGY 31
 Db 108 TWEASKRSYQFWDTPQVPLGEVNVTHGVPDPKDNIRQEPYTLPGF 156
 RESULT 15
 NMT1_MOUSE
 ID NMT1_MOUSE STANDARD; PRT; 496 AA.
 AC 070310;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (peptide N-
 DE myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase
 DE 1) (NMT 1) (Type I N-myristoyltransferase).
 GN NMT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=98175914; PubMed=9506952;
 RA Giang D.K., Cravatt B.F.;
 RA "A second mammalian N-myristoyltransferase.";
 RL J. Biol. Chem. 273:6595-6598(1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

Search completed: October 14, 2003, 08:39:11
Job time : 11.9636 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:36:06 ; Search time 41.5682 Seconds
(without alignments)
192.446 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.podent.*
- 12: sp.virus.*
- 13: sp.vertibrate.*
- 14: sp.unclassified.*
- 15: sp.rvirus.*
- 16: sp.bacteriap.*
- 17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	146	89.6	188	6 Q95KP0	Q95kp0 bos taurus
2	138	84.7	27	6 Q9TRZ6	Q9trz6 sus scrofa
3	58.5	35.9	189	16 Q8XA03	Q8xa03 escherichia
4	58	35.6	430	10 Q23846	Q23846 brassica ol
5	56	34.4	367	10 Q9SEB5	Q9seb5 hirschielfidi
6	56	34.4	431	10 Q23849	Q23849 brassica ca
7	55	33.7	368	10 Q9SBP2	Q9sbp2 raphanus ra
8	55	33.7	421	10 Q8S9B2	Q8s9b2 brassica ol
9	54	33.1	373	16 Q9K6R4	Q9k6r4 bacillus ha
10	53	32.5	346	5 Q9BIA5	Q9bia5 caenorhabdi
11	53	32.5	357	5 Q9BIA9	Q9bia9 caenorhabdi
12	53	32.5	430	10 Q8H0C3	Q8h0c3 brassica na
13	52	31.9	428	10 Q23839	Q23839 brassica ol
14	52	31.9	507	12 Q56958	Q56958 human papil
15	52	31.9	775	2 Q8L163	Q8l163 thermoanaer
16	52	31.9	963	11 Q8K0C1	Q8k0c1 mus musculu

17 52 31.9 1004 2 Q8GHM6
18 51.5 31.6 620 16 Q8G3H2
19 51 31.3 161 2 Q9S412
20 51 31.3 418 10 Q39280
21 51 31.3 428 10 Q80351
22 51 31.3 429 10 Q23843
23 51 31.3 857 10 Q39392
24 51 31.3 859 10 Q9MB87
25 51 31.3 892 5 Q9V3Z4
26 51 31.3 898 5 Q8MSU8
27 50 30.7 90 10 Q9M9R8
28 50 30.7 425 10 Q8S9B0
29 50 30.7 427 10 Q23859
30 50 30.7 428 10 Q23857
31 50 30.7 436 10 Q9SAZ7
32 50 30.7 653 16 Q984T6
33 50 30.7 846 10 Q9ZNM9
34 50 30.7 860 10 Q9ZNM6
35 50 30.7 1181 4 Q96JV0
36 50 30.7 1412 4 Q96JM2
37 49.5 30.4 167 8 Q951T7
38 49.5 30.4 167 8 Q951T9
39 49.5 30.4 167 8 Q94P28
40 49.5 30.4 167 8 Q951U0
41 49.5 30.4 167 8 Q951T8
42 49.5 30.4 227 8 Q958G9
43 49.5 30.4 352 10 Q9LJ66
44 49 30.1 59 17 Q97AP4
45 49 30.1 397 10 Q8LCQ2

ALIGNMENTS

RESULT 1

Q95KP0 PRELIMINARY; PRT; 188 AA.
ID Q95KP0
AC Q95KP0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adrenomedullin.
GN PBAM-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
RA Kangawa K., Eto T.;
RT "ADRENOMEDULLIN (11-26): AN ENDOGENOUS HYPERTENSIVE PEPTIDE ISOLATED FROM BOVINE ADRENAL MEDULLA.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB055107; BAB62176.1; -
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
DR PRINTS; PR00801; ADRENOMEDULLIN.
SQ SEQUENCE 188 AA; 20963 MW; 6102E69A756DCA86 CRC64;

Query Match 89.6%; Score 146; DB 6; Length 188;
Best Local Similarity 90.3%; Pred. No. 3e-13;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31
Db 116 TVQKLAHQIYHFTDKDKGSAFRSKISPOGY 146

RESULT 2

Q9TRZ6 PRELIMINARY; PRT; 27 AA.
ID Q9TRZ6

RA Luu D.T., Hugues S., Passelegue E., Heizmann P.;
RT "Evidence for orthologous S-locus-related I genes in several genera of

RT Brassicaceae.";
 RL Mol. Gen. Genet. 264:735-745(2001).
 DR EMBL; AF162909; AAF22268.1; -;
 DR InterPro; IPR001480; B_lectin.
 DR InterPro; IPR000858; Slocus_glycop.
 DR Pfam; PF01453; Agglutinin; 1.
 DR Pfam; PF00954; S_locus_glycop; 1.
 DR SMART; SM00108; B_lectin; 1.
 FT NON_TER 1
 FT NON_TER 367
 SQ SEQUENCE 367 AA; 41676 MW; 48943E2EA85A2E45 CRC64;
 Query Match 34.4%; Score 56; DB 10; Length 367;
 Best Local Similarity 28.2%; Pred. No. 7.6;
 Matches 11; Conservative 9; Mismatches 9; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : : : : : : : : : :
 Db 194 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKISSG 232
 ||||: : ||| : : : : : : : : : : : : : :
 RESULT 6
 Q23849 PRELIMINARY; PRT; 431 AA.
 ID O23849
 AC O23849
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE S glycoprotein (Fragment).
 OS Brassica campestris (Field mustard).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3711;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=97352858; PubMed=9207151;
 KUSABA M., NISHIO T., SATTA Y., HINATA K., OKENDON D.;
 "Striking sequence similarity in inter- and intra-specific comparisons
 of class I SLG alleles from Brassica oleracea and Brassica
 campestris: implications for the evolution and recognition
 mechanism.";
 Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).
 EMBL; D85215; BAA21949.1; -;
 InterPro; IPR001480; B_lectin.
 InterPro; IPR003609; Pan_app.
 InterPro; IPR000858; Slocus_glycop.
 Pfam; PF01453; Agglutinin; 1.
 Pfam; PF00954; S_locus_glycop; 1.
 SMART; SM00108; B_lectin; 1.
 SMART; SM00473; PAN_AP; 1.
 NON_TER 1
 NON_TER 431
 SQ SEQUENCE 431 AA; 49227 MW; BED2FAF8C3CD4B5 CRC64;
 Query Match 34.4%; Score 56; DB 10; Length 431;
 Best Local Similarity 30.8%; Pred. No. 9;
 Matches 12; Conservative 8; Mismatches 9; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : : : : : : : : : :
 Db 232 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKISSG 270
 ||||: : ||| : : : : : : : : : : : : : :
 RESULT 7
 Q9SBP2 PRELIMINARY; PRT; 368 AA.
 ID Q9SBP2
 AC Q9SBP2
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE S-locus related (Fragment).
 OS SLR.
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : : : : : : : : : :
 Db 232 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKISSG 270
 ||||: : ||| : : : : : : : : : : : : : :
 RESULT 8
 Q8S9B2 PRELIMINARY; PRT; 421 AA.
 ID Q8S9B2
 AC Q8S9B2
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE S receptor kinase (Fragment).
 GN SRK
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3712;
 [1]
 SEQUENCE FROM N.A.
 Kimura R., Sato K., Fujimoto R., Nishio T.;
 "Recognition specificity of self-incompatibility maintained after the
 divergence of Brassica oleracea and Brassica rapa.";
 Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 EMBL; AB070624; BAB86338.1; -;
 InterPro; IPR001480; B_lectin.
 InterPro; IPR003014; PAN.
 InterPro; IPR003609; Pan_app.
 InterPro; IPR000858; Slocus_glycop.
 Pfam; PF01453; Agglutinin; 1.
 Pfam; PF00024; PAN; 1.
 Pfam; PF00954; S_locus_glycop; 1.
 SMART; SM00108; B_lectin; 1.
 SMART; SM00473; PAN_AP; 1.
 Receptor; Kinase.
 NON_TER 1
 NON_TER 421
 SQ SEQUENCE 421 AA; 48015 MW; 835E29608FC9F160 CRC64;
 Query Match 33.7%; Score 55; DB 10; Length 421;
 Best Local Similarity 30.8%; Pred. No. 12;
 Matches 12; Conservative 8; Mismatches 9; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : : : : : : : : : :
 Db 195 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKISSG 233
 ||||: : ||| : : : : : : : : : : : : : :
 RESULT 9
 Q8S9B2 PRELIMINARY; PRT; 421 AA.
 ID Q8S9B2
 AC Q8S9B2
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE S receptor kinase (Fragment).
 GN SRK
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3712;
 [1]
 SEQUENCE FROM N.A.
 Kimura R., Sato K., Fujimoto R., Nishio T.;
 "Recognition specificity of self-incompatibility maintained after the
 divergence of Brassica oleracea and Brassica rapa.";
 Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 EMBL; AB070624; BAB86338.1; -;
 InterPro; IPR001480; B_lectin.
 InterPro; IPR003014; PAN.
 InterPro; IPR003609; Pan_app.
 InterPro; IPR000858; Slocus_glycop.
 Pfam; PF01453; Agglutinin; 1.
 Pfam; PF00024; PAN; 1.
 Pfam; PF00954; S_locus_glycop; 1.
 SMART; SM00108; B_lectin; 1.
 SMART; SM00473; PAN_AP; 1.
 Receptor; Kinase.
 NON_TER 1
 NON_TER 421
 SQ SEQUENCE 421 AA; 48015 MW; 835E29608FC9F160 CRC64;
 Query Match 33.7%; Score 55; DB 10; Length 368;
 Best Local Similarity 28.2%; Pred. No. 11;
 Matches 11; Conservative 10; Mismatches 8; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : : : : : : : : : :
 Db 195 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKISSG 233
 ||||: : ||| : : : : : : : : : : : : : :
 RESULT 10
 Q8S9B2 PRELIMINARY; PRT; 421 AA.
 ID Q8S9B2
 AC Q8S9B2
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE S receptor kinase (Fragment).
 GN SRK
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3712;
 [1]
 SEQUENCE FROM N.A.
 Kimura R., Sato K., Fujimoto R., Nishio T.;
 "Recognition specificity of self-incompatibility maintained after the
 divergence of Brassica oleracea and Brassica rapa.";
 Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 EMBL; AB070624; BAB86338.1; -;
 InterPro; IPR001480; B_lectin.
 InterPro; IPR003014; PAN.
 InterPro; IPR003609; Pan_app.
 InterPro; IPR000858; Slocus_glycop.
 Pfam; PF01453; Agglutinin; 1.
 Pfam; PF00024; PAN; 1.
 Pfam; PF00954; S_locus_glycop; 1.
 SMART; SM00108; B_lectin; 1.
 SMART; SM00473; PAN_AP; 1.
 Receptor; Kinase.
 NON_TER 1
 NON_TER 421
 SQ SEQUENCE 421 AA; 48015 MW; 835E29608FC9F160 CRC64;
 Query Match 33.7%; Score 55; DB 10; Length 368;
 Best Local Similarity 28.2%; Pred. No. 11;
 Matches 11; Conservative 10; Mismatches 8; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : : : : : : : : : :
 Db 195 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKISSG 233

RT Brassicaceae.";
 RL Mol. Gen. Genet. 264:735-745(2001).
 DR EMBL; AF162909; AAF22268.1; -.
 DR InterPro; IPR001480; B_lectin.
 DR InterPro; IPR000858; Slocus_glycop.
 DR Pfam; PF01453; Agglutinin; 1.
 DR Pfam; PF00954; S_locus_glycop; 1.
 DR SMART; SM00108; B_lectin; 1.
 FT NON_TER 1
 FT NON_TER 367
 SQ SEQUENCE 367 AA; 41676 MW; 48943E2EA85A2E45 CRC64;
 Query Match 34.4%; Score 56; DB 10; Length 367;
 Best Local Similarity 28.2%; Pred. No. 7.6;
 Matches 11; Conservative 9; Mismatches 9; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 194 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKVSDDGY 232
 ||||: : ||| : : : : : ||
 RESULT 6
 Q23849 PRELIMINARY; PRT; 431 AA.
 ID O23849
 AC O23849
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE S glycoprotein (Fragment).
 OS Brassica campestris (Field mustard).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3711;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=97352858; PubMed=9207151;
 KUSABA M., NISHIO T., SATTA Y., HINATA K., OKENDON D.;
 "Striking sequence similarity in inter- and intra-specific comparisons
 of class I SLG alleles from Brassica oleracea and Brassica
 campestris: implications for the evolution and recognition
 mechanism.";
 Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).
 EMBL; D85215; BAA21949.1; -.
 DR InterPro; IPR001480; B_lectin.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR000858; Slocus_glycop.
 DR Pfam; PF01453; Agglutinin; 1.
 DR Pfam; PF00954; S_locus_glycop; 1.
 DR SMART; SM00108; B_lectin; 1.
 DR SMART; SM00473; PAN_AP; 1.
 FT NON_TER 1
 FT NON_TER 431
 SQ SEQUENCE 431 AA; 49227 MW; BED2FAF8C3CD4B5 CRC64;
 Query Match 34.4%; Score 56; DB 10; Length 431;
 Best Local Similarity 30.8%; Pred. No. 9;
 Matches 12; Conservative 8; Mismatches 9; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 232 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKVSDDGY 270
 ||||: : ||| : : : : : ||
 RESULT 7
 Q9SBP2 PRELIMINARY; PRT; 368 AA.
 ID Q9SBP2
 AC Q9SBP2
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE S-locus related (Fragment).
 OS SLR.
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 232 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKVSDDGY 270
 ||||: : ||| : : : : : ||
 RESULT 8
 Q8S9B2 PRELIMINARY; PRT; 421 AA.
 ID Q8S9B2
 AC Q8S9B2
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE S receptor kinase (Fragment).
 GN SRK
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3712;
 [1]
 SEQUENCE FROM N.A.
 Kimura R., Sato K., Fujimoto R., Nishio T.;
 "Recognition specificity of self-incompatibility maintained after the
 divergence of Brassica oleracea and Brassica rapa.";
 Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB070624; BAB86338.1; -.
 DR InterPro; IPR001480; B_lectin.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR000858; Slocus_glycop.
 DR Pfam; PF01453; Agglutinin; 1.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00954; S_locus_glycop; 1.
 DR SMART; SM00108; B_lectin; 1.
 DR SMART; SM00473; PAN_AP; 1.
 DR Receptor; Kinase.
 FT NON_TER 1
 FT NON_TER 421
 SQ SEQUENCE 421 AA; 48015 MW; 835E29608FC9F160 CRC64;
 Query Match 33.7%; Score 55; DB 10; Length 421;
 Best Local Similarity 30.8%; Pred. No. 12;
 Matches 12; Conservative 8; Mismatches 9; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 195 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKVSDDGY 233
 ||||: : ||| : : : : : ||
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 195 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKVSDDGY 233
 ||||: : ||| : : : : : ||
 RESULT 8
 Q8S9B2 PRELIMINARY; PRT; 421 AA.
 ID Q8S9B2
 AC Q8S9B2
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE S receptor kinase (Fragment).
 GN SRK
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3712;
 [1]
 SEQUENCE FROM N.A.
 Kimura R., Sato K., Fujimoto R., Nishio T.;
 "Recognition specificity of self-incompatibility maintained after the
 divergence of Brassica oleracea and Brassica rapa.";
 Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB070624; BAB86338.1; -.
 DR InterPro; IPR001480; B_lectin.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR000858; Slocus_glycop.
 DR Pfam; PF01453; Agglutinin; 1.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00954; S_locus_glycop; 1.
 DR SMART; SM00108; B_lectin; 1.
 DR SMART; SM00473; PAN_AP; 1.
 DR Receptor; Kinase.
 FT NON_TER 1
 FT NON_TER 421
 SQ SEQUENCE 421 AA; 48015 MW; 835E29608FC9F160 CRC64;
 Query Match 33.7%; Score 55; DB 10; Length 368;
 Best Local Similarity 28.2%; Pred. No. 11;
 Matches 11; Conservative 10; Mismatches 8; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 195 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKVSDDGY 233
 ||||: : ||| : : : : : ||
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 195 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKVSDDGY 233
 ||||: : ||| : : : : : ||
 Query Match 33.7%; Score 55; DB 10; Length 368;
 Best Local Similarity 28.2%; Pred. No. 11;
 Matches 11; Conservative 10; Mismatches 8; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 195 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKVSDDGY 233
 ||||: : ||| : : : : : ||
 Query Match 33.7%; Score 55; DB 10; Length 368;
 Best Local Similarity 28.2%; Pred. No. 11;
 Matches 11; Conservative 10; Mismatches 8; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 195 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKVSDDGY 233
 ||||: : ||| : : : : : ||
 Query Match 33.7%; Score 55; DB 10; Length 368;
 Best Local Similarity 28.2%; Pred. No. 11;
 Matches 11; Conservative 10; Mismatches 8; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 195 QKLSVMYVNFENSEEVAYTFRTNNSIYSLKVSDDGY 233
 ||||: : ||| : : : : : ||
 Query Match 33.7%; Score 55; DB 10; Length 368;
 Best Local Similarity 28.2%; Pred. No. 11;
 Matches 11; Conservative 10; Mismatches 8; Indels 10; Gaps 1;
 QY 3 OKLAHQIYQFTDKDKD-----NVAPRSKISPGY 31
 ||||: : ||| : : : : : ||
 Db 1

Db 227 QKLSYMYNFTDNSEVAYFTLMTNNSFYSRLKLSSEGY 265

RESULT 9

Q9K6R4
ID Q9K6R4 PRELIMINARY; PRT; 373 AA.
AC Q9K6R4
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-WAR-2003 (TReMBLrel. 23, Last annotation update)
DE Lipopolysaccharide biosynthesis.
GN BH3663.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
RA "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001519; BAB07382.1; -.
DR InterPro; IPR001296; Glyco_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 42062 MW; 0C67C2C98CBA4107 CRC64;

Query Match 33.1%; Score 54; DB 16; Length 373;

Best Local Similarity 48.0%; Pred. No. 15;

Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 VOKLAHQIYQFTDKDKNVAPRSKI 26

Db 132 VYKLAHQIYSLSEGKENVRRYKI 156

RESULT 10

Q9BIA5
ID Q9BIA5 PRELIMINARY; PRT; 346 AA.
AC Q9BIA5
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 39.7 kDa protein.
GN C17C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z.;
RT "The sequence of C. elegans cosmid C17C3.";
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41279; AAK31428.1; -.
DR HSSP; P23911; 1C8U.
DR WormPep; C17C3.1a; CE27070.
DR InterPro; IPR003703; Acyl_CoA_thio.
DR Pfam; PF02551; Acyl_CoA_thio; 2.
DR TIGRFAMS; TIGR00189; tesB; 1.
KW Hypothetical protein.
SQ SEQUENCE 357 AA; 41046 MW; D62561FC872C1158 CRC64;

Query Match 32.5%; Score 53; DB 5; Length 357;

Best Local Similarity 40.0%; Pred. No. 20;

Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 OKLAHQIYQFTDKDKNVAP 22

Db 48 QEIAHKFFDTLKKDSFSP 67

RESULT 12

Q8H0C3
ID Q8H0C3 PRELIMINARY; PRT; 430 AA.
AC Q8H0C3

DR EMBL; U41279; AAK31429.1; -.
DR HSSP; P23911; 1C8U
DR WormPep; C17C3.1b; CE27071.
DR InterPro; IPR003703; Acyl_CoA_thio.
DR Pfam; PF02551; Acyl_CoA_thio; 2.
DR TIGRFAMS; TIGR00189; tesB; 1.
KW Hypothetical protein.
SQ SEQUENCE 346 AA; 39688 MW; CF853F9CAF0B93B2 CRC64;

Query Match 32.5%; Score 53; DB 5; Length 346;

Best Local Similarity 40.0%; Pred. No. 19;

Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 OKLAHQIYQFTDKDKNVAP 22

Db 37 QEIAHKFFDTLKKDSFSP 56

RESULT 11

Q9BIA9
ID Q9BIA9 PRELIMINARY; PRT; 357 AA.
AC Q9BIA9
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 41.0 kDa protein.
GN C17C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z.;
RT "The sequence of C. elegans cosmid C17C3.";
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41279; AAK31428.1; -.
DR HSSP; P23911; 1C8U.
DR WormPep; C17C3.1a; CE27070.
DR InterPro; IPR003703; Acyl_CoA_thio.
DR Pfam; PF02551; Acyl_CoA_thio; 2.
DR TIGRFAMS; TIGR00189; tesB; 1.
KW Hypothetical protein.
SQ SEQUENCE 357 AA; 41046 MW; D62561FC872C1158 CRC64;

Query Match 32.5%; Score 53; DB 5; Length 357;

Best Local Similarity 40.0%; Pred. No. 20;

Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 OKLAHQIYQFTDKDKNVAP 22

Db 48 QEIAHKFFDTLKKDSFSP 67

RESULT 12

Q8H0C3
ID Q8H0C3 PRELIMINARY; PRT; 430 AA.
AC Q8H0C3

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DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE S-locus glycoprotein (Fragment).
GN SLG.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RA Odashima M., Okamoto S., Nishio T.;
RL "Distribution of S haplotypes in Brassica napus.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AB086974; BAC53782.1; -
FT NON_TER 1 430
FT NON_TER 430 430
SQ SEQUENCE 430 AA; 49065 MW; 60152ED337CD0928 CRC64;

Query Match 32.5%; Score 53; DB 10; Length 430;
Best Local Similarity 25.6%; Pred. No. 25;
Matches 10; Conservative 10; Mismatches 9; Indels 10; Gaps 1;

QY 3 QKLAHQIYQFTDKD-----NVAPRSKISPGY 31
||| : : || : : : : || : :
Db 230 QKLGWVYNFTENSEVAYTFRITNNSIYRLKVSSEGF 268

RESULT 13
O23839
ID O23839 PRELIMINARY; PRT; 428 AA.
AC O23839;
DT 01-JAN-1998 (TremBLrel. 05, Created)
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE S glycoprotein (Fragment).
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RA Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.;
RL "Striking sequence similarity in inter- and intra-specific comparisons
of class I SLG alleles from Brassica oleracea and Brassica
campestris: Implications for the evolution and recognition
mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).
DR EMBL: D85205; BAA21939.1; -.
DR InterPro: IPR001480; B_lectin.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR000858; Slocus_glycop.
DR Pfam: PF01453; Agglutinin; 1.
DR Pfam: PF00954; S_lectin; 1.
DR SMART: SM00108; B_lectin; 1.
DR SMART: SM00473; PAN_AP; 1.
FT NON_TER 1 428
FT NON_TER 428 428
SQ SEQUENCE 428 AA; 48724 MW; 18E04542C7293BEA CRC64;

Query Match 31.9%; Score 52; DB 10; Length 428;
Best Local Similarity 28.2%; Pred. No. 34;
Matches 11; Conservative 8; Mismatches 10; Indels 10; Gaps 1;

QY 3 QKLAHQIYQFTDKD-----NVAPRSKISPGY 31
||| : : || : : : : || : :
Db 229 QKLSYVYNFTENSEVAYTFRITNNSIYRLKVSDDGY 267

RESULT 14

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O56958
ID O56958 PRELIMINARY; PRT; 507 AA.
AC O56958;
DT 01-JUN-1998 (TremBLrel. 06, Created)
DT 01-JUN-1998 (TremBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE E6, E7, E1, E2, E4, E12, and L1 genes.
GN L1.
OS Human papillomavirus type 80.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=69987;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98118461; PubMed=9454709;
RA Bellus H., Saegling B., Bergmann K., Shananin V., de Villiers E.M.;
RL "The genomes of three of four novel HPV types, defined by differences
of their L1 genes, show high conservation of the E7 gene and the
UTR.";
RL Virology 240:359-365(1998).
DR EMBL: Y15176; CAA75476.1; -.
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1; 1.
DR PRINTS: PR00865; HPV_CAPSID_L1.
DR PRODOM: PD000544; PV_capsid_L1; 1.
SQ SEQUENCE 507 AA; 56998 MW; 6F17589CC91004F6 CRC64;

Query Match 31.9%; Score 52; DB 12; Length 507;
Best Local Similarity 38.2%; Pred. No. 41;
Matches 13; Conservative 3; Mismatches 14; Indels 4; Gaps 1;

QY 1 TVQKLAHQIYQFTD-----KDKDNVAPRSKISPG 30
||| : : || : : : : || : :
Db 420 TPDNAVHDIYRIDSKATKCPDAVPKDKEDPFG 453

RESULT 15
O8L163
ID O8L163 PRELIMINARY; PRT; 775 AA.
AC O8L163;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Kojibiose phosphorylase.
GN KOJP.
OS Thermoanaerobacter brockii (Thermoanaerobium brockii).
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=29323;
RN [1]
RP SEQUENCE FROM N.A.
RA Maruta K., Mukai K., Kubota M., Chaen H., Fukuda S., Kurimoto M.;
RL "The genes encoding a trehalose phosphorylase and a kojibiose
phosphorylase from Thermoanaerobacter brockii ATCC35047.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AB073931; BAB97300.1; -.
DR InterPro: IPR005194; Glyco_hydro_65C.
DR InterPro: IPR005195; Glyco_hydro_65M.
DR InterPro: IPR005196; Glyco_hydro_65N.
DR Pfam: PF03633; Glyco_hydro_65C; 1.
DR Pfam: PF03632; Glyco_hydro_65M; 1.
DR Pfam: PF03636; Glyco_hydro_65N; 1.
SQ SEQUENCE 775 AA; 89700 MW; FB9760F02B220E56 CRC64;

Query Match 31.9%; Score 52; DB 2; Length 775;
Best Local Similarity 36.0%; Pred. No. 65;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 6 AHQIYQFTDKDNVAPRSKISPG 30
||| : : || : : : : || : :
Db 217 AVRLHYEDKEKNNAIKFRFLPLG 241

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Search completed: October 14, 2003, 08:40:19
Job time : 44.5682 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:37:31 ; Search time 20.4318 Seconds
(without alignments)
64.196 Million cell updates/sec

Title: US-09-931-700-3

Perfect score: 163

Sequence: 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA.*
- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	163	100.0	31	3	US-09-070-504-23
2	163	100.0	31	4	US-09-011-922A-3
3	163	100.0	31	4	US-09-011-922A-14
4	163	100.0	31	4	US-09-280-501-9
5	163	100.0	38	4	US-09-280-501-6
6	163	100.0	40	4	US-09-280-501-11
7	163	100.0	52	3	US-09-070-504-14
8	163	100.0	185	1	US-08-233-389C-1
9	163	100.0	185	2	US-08-801-863-1
10	163	100.0	185	2	US-08-486-596A-1
11	163	100.0	185	4	US-09-004-713-1
12	158	96.9	30	4	US-09-280-501-5
13	157	96.3	188	1	US-08-233-389C-3
14	157	96.3	188	2	US-08-801-863-3
15	157	96.3	188	2	US-08-486-596A-3
16	157	96.3	188	2	US-09-004-713-3
17	154	94.5	29	4	US-09-280-501-4
18	150	92.0	40	4	US-09-280-501-8
19	150	92.0	50	4	US-09-280-501-7
20	149	91.4	28	4	US-09-280-501-3
21	146	90.8	50	3	US-09-070-504-15
22	144	88.3	27	4	US-09-280-501-2
23	140	85.9	26	4	US-09-280-501-1
24	123	75.5	23	4	US-09-280-501-17
25	112	68.7	21	4	US-09-280-501-16
26	74	45.4	13	4	US-09-280-501-15
27	68	41.7	13	4	US-09-280-501-10

28	57	35.0	13	4	US-09-011-922A-2	Sequence 2, Appli
29	52	31.9	775	3	US-08-966-388-4	Sequence 4, Appli
30	52	31.9	775	3	US-09-188-403-4	Sequence 4, Appli
31	52	31.9	775	3	US-09-188-404-4	Sequence 4, Appli
32	52	31.9	775	3	US-09-281-259-4	Sequence 4, Appli
33	52	31.9	1005	4	US-09-252-931A-24655	Sequence 24655, A
34	51	31.3	10	2	US-08-934-222-17	Sequence 17, Appli
35	51	31.3	10	2	US-08-933-402-17	Sequence 17, Appli
36	51	31.3	10	2	US-09-207-621-17	Sequence 17, Appli
37	51	31.3	10	2	US-08-532-818-17	Sequence 17, Appli
38	51	31.3	10	3	US-09-231-797-17	Sequence 17, Appli
39	51	31.3	10	3	US-08-934-224-17	Sequence 17, Appli
40	51	31.3	10	3	US-08-933-843-17	Sequence 17, Appli
41	51	31.3	10	3	US-08-934-223-17	Sequence 17, Appli
42	51	31.3	10	3	US-09-413-492-17	Sequence 17, Appli
43	50	30.7	9	4	US-09-280-501-14	Sequence 14, Appli
44	48	29.4	478	4	US-09-786-240-31	Sequence 31, Appli
45	47	28.8	858	2	US-08-265-628-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-23

Query Match 100.0%; Score 163; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

Db 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

RESULT 2
 US-09-011-922A-3
 ; Sequence 3, Application US/09011922A
 ; Patent No. 6320022
 ; GENERAL INFORMATION:
 ; APPLICANT: Cuttitta, Frank; Martinez,
 ; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
 ; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
 ; APPLICANT: Karen; Macri, Charles
 ; TITLE OF INVENTION: Functional Role of
 ; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
 ; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
 ; TITLE OF INVENTION: Physiology
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 ; STREET: 345 Park Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10154-0053
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: MS WORD 97
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/011.922A
 ; FILING DATE: 17-Feb-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/60/002,514
 ; FILING DATE: 18-Aug-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/60/002,936
 ; FILING DATE: 30-Aug-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/60/013,172
 ; FILING DATE: 12-Mar-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/13286
 ; FILING DATE: 16-Aug-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Leslie A. Serunian
 ; REGISTRATION NUMBER: 35,353
 ; REFERENCE/DOCKET NUMBER: 2026-4202US3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4800
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FEATURE:
 ; NAME/KEY: P072
 ; OTHER INFORMATION: PreproAM(116-146)
 US-09-011-922A-3

Query Match 100.0%; Score 163; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.4e-19;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
 DB 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 3
 US-09-011-922A-14

; Sequence 14, Application US/09011922A
 ; Patent No. 6320022
 ; GENERAL INFORMATION:
 ; APPLICANT: Cuttitta, Frank; Martinez,
 ; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
 ; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
 ; APPLICANT: Karen; Macri, Charles
 ; TITLE OF INVENTION: Functional Role of
 ; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
 ; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
 ; TITLE OF INVENTION: Physiology
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 ; STREET: 345 Park Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10154-0053
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: MS WORD 97
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/011.922A
 ; FILING DATE: 17-Feb-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/60/002,514
 ; FILING DATE: 18-Aug-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/60/002,936
 ; FILING DATE: 30-Aug-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/60/013,172
 ; FILING DATE: 12-Mar-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/13286
 ; FILING DATE: 16-Aug-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Leslie A. Serunian
 ; REGISTRATION NUMBER: 35,353
 ; REFERENCE/DOCKET NUMBER: 2026-4202US3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4800
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic homolog of
 ; OTHER INFORMATION: two-thirds of the intact AM peptide
 US-09-011-922A-14

Query Match 100.0%; Score 163; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.4e-19;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
 DB 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 4
 US-09-280-501-9
 ; Sequence 9, Application US/09280501
 ; Patent No. 6440421
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooper, Garth James Smith

US-09-280-501-11
 ; Sequence 11, Application US/09280501
 ; Patent No. 6440421
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooper, Garth James Smith
 ; APPLICANT: Reid, Ian Reginald
 ; APPLICANT: Cornish, Jillian
 ; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
 ; TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
 ; FILE REFERENCE: 09897-005001
 ; CURRENT APPLICATION NUMBER: US/09/280,501
 ; CURRENT FILING DATE: 1999-03-30
 ; PRIOR APPLICATION NUMBER: 08/634,562
 ; PRIOR FILING DATE: 1996-04-18

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; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,389C
; FILING DATE: 26-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-233-389C-1

Query Match 100.0%; Score 163; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146

RESULT 9
US-08-801-863-1
; Sequence 1, Application us/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,863
; FILING DATE: CONCURRENTLY HERewith
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; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-863-1

Query Match 100.0%; Score 163; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146

RESULT 10
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-596A-1

Query Match 100.0%; Score 163; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146
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Db      116 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146

RESULT 11
US-09-004-713-1
; Sequence 1, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/004,713
; FILING DATE: JANUARY 7, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-004-713-1

Query Match      100.0%; Score 163; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
      116 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146

RESULT 12
US-09-280-501-5
; Sequence 5, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30

Query Match      96.3%; Score 157; DB 1; Length 188;
Best Local Similarity 96.8%; Pred. No. 2e-17;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
      116 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146

RESULT 13
US-08-233-389C-3
; Sequence 3, Application US/08233389C
; Patent No. 5639655
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,389C
; FILING DATE: 26-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-233-389C-3

Query Match      96.3%; Score 157; DB 1; Length 188;
Best Local Similarity 96.8%; Pred. No. 2e-17;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
      116 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146

RESULT 14
US-08-801-863-3
; Sequence 3, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
```

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; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,863
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-863-3

Query Match          96.3%; Score 157; DB 2; Length 188;
Best Local Similarity 96.8%; Pred. No. 2e-17;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
Db 116 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 146

RESULT 15
US-08-486-596A-3
; Sequence 3, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAHURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-596A-3
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Query Match          96.3%; Score 157; DB 2; Length 188;
Best Local Similarity 96.8%; Pred. No. 2e-17;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
Db 116 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 146
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:40:27 ; Search time 62 seconds
(without alignments)
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Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQTDKDKDNVPRSKISPGY 31

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	100.0	31	9 US-09-931-700-3	Sequence 3, Appli
2	163	100.0	31	9 US-09-931-700-14	Sequence 14, Appl
3	163	100.0	31	9 US-09-813-345-23	Sequence 23, Appl
4	163	100.0	52	9 US-09-813-345-14	Sequence 14, Appl
5	163	100.0	52	15 US-10-197-954-2	Sequence 2, Appli
6	148	90.8	50	9 US-09-813-345-15	Sequence 15, Appl
7	57	35.0	13	9 US-09-931-700-2	Sequence 2, Appli
8	48	29.4	478	12 US-10-427-631-31	Sequence 31, Appl
9	48	29.4	1745	12 US-09-795-061-4	Sequence 4, Appli
10	47.5	29.1	984	15 US-10-128-714-3547	Sequence 3547, Ap
11	47.5	29.1	1058	15 US-10-128-714-8547	Sequence 8547, Ap
12	47	28.8	33	9 US-09-864-761-43882	Sequence 43882, A
13	47	28.8	327	15 US-10-102-806-570	Sequence 570, App
14	46.5	28.5	131	12 US-09-903-190-174	Sequence 174, Appl
15	46	28.2	608	12 US-09-738-269-41	Sequence 41, Appl

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16 46 28.2 14 US-10-023-437-41 Sequence 41, Appl
17 45 27.6 11 US-09-791-279-219 Sequence 219, App
18 45 27.6 12 US-10-269-017-1 Sequence 1, Appli
19 44.5 27.3 281 US-10-352-393-5 Sequence 5, Appli
20 44.5 27.3 293 US-10-032-585-7130 Sequence 7130, Ap
21 44 27.0 12 US-09-882-227-180 Sequence 180, App
22 44 27.0 9 US-09-846-729A-3 Sequence 3, Appli
23 44 27.0 462 US-09-846-729A-17 Sequence 17, Appli
24 44 27.0 462 US-10-441-667-3 Sequence 3, Appli
25 44 27.0 462 US-10-441-667-17 Sequence 17, Appli
26 44 27.0 484 US-09-846-729A-14 Sequence 14, Appli
27 44 27.0 464 US-10-441-667-14 Sequence 14, Appli
28 44 27.0 478 US-10-078-866-2 Sequence 2, Appli
29 44 27.0 483 US-10-439-533-2 Sequence 2, Appli
30 43.5 26.7 175 US-10-216-163-74 Sequence 74, Appli
31 43.5 26.7 175 US-10-218-765-74 Sequence 74, Appli
32 43.5 26.7 175 US-10-219-066-74 Sequence 74, Appli
33 43.5 26.7 175 US-10-219-066-74 Sequence 74, Appli
34 43.5 26.7 175 US-10-219-067-74 Sequence 74, Appli
35 43.5 26.7 175 US-10-219-068-74 Sequence 74, Appli
36 43.5 26.7 175 US-10-219-069-74 Sequence 74, Appli
37 43.5 26.7 175 US-10-219-073-74 Sequence 74, Appli
38 43.5 26.7 175 US-10-219-475-74 Sequence 74, Appli
39 43.5 26.7 175 US-10-219-480-74 Sequence 74, Appli
40 43.5 26.7 175 US-10-219-483-74 Sequence 74, Appli
41 43.5 26.7 175 US-10-219-525-74 Sequence 74, Appli
42 43.5 26.7 175 US-10-219-526-74 Sequence 74, Appli
43 43.5 26.7 175 US-10-219-530-74 Sequence 74, Appli
44 43.5 26.7 175 US-10-219-531-74 Sequence 74, Appli
45 43.5 26.7 175 US-10-219-532-74 Sequence 74, Appli

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ALIGNMENTS

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RESULT 1
US-09-931-700-3
; Sequence 3, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CATTIITA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; FILE REFERENCE: 2026-4202USA
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide, p072,
; OTHER INFORMATION: PreproAM (amino acids 116-146)

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US-09-931-700-3

Query Match 100.0%; Score 163; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 2

US-09-931-700-14
; Sequence 14, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202US4
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 31
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide,
; OTHER INFORMATION: Synthetic homolog of AM (P072), Structural amino
; OTHER INFORMATION: acid sequence representing two-thirds of the
; OTHER INFORMATION: intact AM peptide
US-09-931-700-14

Query Match 100.0%; Score 163; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
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Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 3

US-09-813-345-23
; Sequence 23, Application US/09813345
; Patent No. US20020068814A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; Saha, Shankar
; Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch & Gebhardt, P.A.
; STREET: 119 No. US20020068814A1th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,345
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-813-345-23

Query Match 100.0%; Score 163; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 4
US-09-813-345-14
; Sequence 14, Application US/09813345
; Patent No. US20020068814A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; Saha, Shankar
; Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch & Gebhardt, P.A.
; STREET: 119 No. US20020068814A1th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,345
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-813-345-14

Query Match 100.0%; Score 163; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.8e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31
DB 22 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 52

RESULT 5

US-10-197-954-2

Sequence 2, Application US/10197954

Publication No. US20030119021A1

GENERAL INFORMATION:

APPLICANT: K*ster, Hubert

APPLICANT: Siddiqi, Suhaib

APPLICANT: Little, Daniel

TITLE OF INVENTION: Capture Compounds, Collections Thereof

TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex

TITLE OF INVENTION: Compositions

FILE REFERENCE: 24743-2305

CURRENT APPLICATION NUMBER: US/10/197,954

CURRENT FILING DATE: 2002-07-16

PRIOR APPLICATION NUMBER: 60/306,019

PRIOR FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 60/314,123

PRIOR FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: 60/363,433

PRIOR FILING DATE: 2002-03-11

NUMBER OF SEQ ID NOS: 149

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 52

TYPE: PRT

ORGANISM: Homo Sapien

US-10-197-954-2

Query Match 100.0%; Score 163; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.8e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31
DB 22 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 52

RESULT 6

US-09-813-345-15

Sequence 15, Application US/09813345

Patent No. US20020068814A1

GENERAL INFORMATION:

APPLICANT: Smith, Derek D.

APPLICANT: Saha, Shankar

APPLICANT: Abel, Peter W.

TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESS: Mueting, Raasch & Gebhardt, P.A.

STREET: 119 No. US20020068814A1th Fourth Street

CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: McCormack, Myra H

REGISTRATION NUMBER: 36,602

REFERENCE/DOCKET NUMBER: 180.00020101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/305-1220

TELEFAX: 612/305-1228

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-813-345-15

Query Match

Best Local Similarity 90.8%; Score 148; DB 9; Length 50;

Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

DB 20 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 50

RESULT 7

US-09-931-700-2

Sequence 2, Application US/09931700

Patent No. US20020055615A1

GENERAL INFORMATION:

APPLICANT: CUTTITTA, FRANK

APPLICANT: MARTINEZ, ALFREDO

APPLICANT: MILLER, MAE JEAN

APPLICANT: UNSWORTH, EDWARD J.

APPLICANT: HOOK, WILLIAM

APPLICANT: WALSH, THOMAS

APPLICANT: GREY, KAREN

APPLICANT: MACRI, CHARLES

TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the

TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and

TITLE OF INVENTION: Physiology

FILE REFERENCE: 2026-4202US4

CURRENT APPLICATION NUMBER: US/09/931,700

CURRENT FILING DATE: 2001-08-16

PRIOR APPLICATION NUMBER: 09/011,922

PRIOR FILING DATE: 1998-02-17

PRIOR APPLICATION NUMBER: PCT/US96/13286

PRIOR FILING DATE: 1996-08-16

PRIOR APPLICATION NUMBER: US/60/013,172

PRIOR FILING DATE: 1996-03-12

PRIOR APPLICATION NUMBER: US60/002,936

PRIOR FILING DATE: 1995-08-30

PRIOR APPLICATION NUMBER: US/60/002,514

PRIOR FILING DATE: 1995-08-18

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Peptide,
OTHER INFORMATION: P071, Ygg-ProproAM (amino acids 122-131)
US-09-931-700-2

Query Match 35.0%; Score 57; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 HQIYQFTDKD 16
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DB 4 HQIYQFTDKD 13

RESULT 8

US-10-427-631-31
Sequence 31, Application US/10427631
Publication No. US20030175923A1

GENERAL INFORMATION:

APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
APPLICANT: BAUGHN, Mariah R.; LAL, Preeti G.;
APPLICANT: YUE, Henry; HILLMAN, Jennifer L.;
APPLICANT: AZIMZAI, Yalda
TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
FILE REFERENCE: PF-0592-1 DIV
CURRENT APPLICATION NUMBER: US/10/427,631
CURRENT FILING DATE: 2003-04-29

PRIOR APPLICATION NUMBER: US 09/786,240
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: PCT/US99/20989
PRIOR FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: US 60/172,220
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: US 60/155,248
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 60/133,642
PRIOR FILING DATE: 1999-05-11
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL Program
SEQ ID NO 31

LENGTH: 478
TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc-feature

OTHER INFORMATION: GenBank ID No. US20030175923A1 g2443814
US-10-427-631-31

Query Match 29.4%; Score 48; DB 12; Length 478;
Best Local Similarity 24.5%; Pred. No. 81;
Matches 12; Conservative 7; Mismatches 12; Indels 18; Gaps 1;

QY 1 TVQKLAHQIYQFTD-----KDKDNVAPRSKISPOQY 31
| : : : | | | | | | | | | |
DB 90 TMEASRSYQFWDTPQVPKLGVEVNHGVPEDKDNIRQEPYTLPGQF 138

RESULT 9

US-09-795-061-4

Sequence 4, Application US/09795061
Publication No. US20030168842A1

GENERAL INFORMATION:

APPLICANT: Greenspan, Daniel S
APPLICANT: Inamura, Yasutada
TITLE OF INVENTION: Pro-Alpha 3(V) Collagen Genes
FILE REFERENCE: 960296.96781
CURRENT APPLICATION NUMBER: US/09/795,061
CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4

LENGTH: 1745

TYPE: PRT

ORGANISM: Homo sapiens

US-09-795-061-4

Query Match 29.4%; Score 48; DB 12; Length 1745;
Best Local Similarity 53.3%; Pred. No. 3.6e+02;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 16 DKDNVAPRSKISPOQ 30
| | | | | : : | | |
DB 223 DCDNLAPAAATVAPOG 237

RESULT 10

US-10-128-714-3547

Sequence 3547, Application US/10128714
Publication No. US20030119013A1

GENERAL INFORMATION:

APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3547
LENGTH: 984
TYPE: PRT

ORGANISM: Aspergillus fumigatus

US-10-128-714-3547

Query Match 29.1%; Score 47.5; DB 15; Length 984;
Best Local Similarity 27.5%; Pred. No. 2.2e+02;
Matches 11; Conservative 10; Mismatches 6; Indels 13; Gaps 1;

QY 3 QKLAHQIYQFTDK-----DKDNVAPRSKISPOQ 29
| : : : | | | | | : : | | | | |
DB 75 QEMAVEIFKTYDRVNMVPRPKLLMIAVDGVAPRAKMQQ 114

RESULT 11

US-10-128-714-8547

Sequence 8547, Application US/10128714
Publication No. US20030119013A1

GENERAL INFORMATION:

APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23

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; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8547
; TYPE: PRT
; LENGTH: 1058
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8547

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Query Match          29.1%; Score 47.5; DB 15; Length 1058;
Best Local Similarity 27.5%; Pred. No. 2.4e+02;
Matches 11; Conservative 10; Mismatches 6; Indels 13; Gaps 1;

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QY      3 QKLAHQIYQFTDK-----DKDNVAPRSKISPG 29
Db      75 QEMVEIFKIDRVNVMVRPKLMLTAVDGVAPKXNQ 114

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RESULT 12
US-09-864-761-43882
; Sequence 43882, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21

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; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43882
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005079.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
; OTHER INFORMATION: EST_HUMAN HIT: A0140742.1, EVALUATE 1.00e-11
US-09-864-761-43882

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```

Query Match          28.8%; Score 47; DB 9; Length 33;
Best Local Similarity 62.5%; Pred. No. 5.3;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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QY      2 VQKLAHQIYQFTDKDK 17
Db      10 VQKLAKENYQFLQTDK 25

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RESULT 13
US-10-102-806-570
; Sequence 570, Application US/10102806
; Publication No. US20030034421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL03P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 570
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-570

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Query Match          28.8%; Score 47; DB 15; Length 327;
Best Local Similarity 41.4%; Pred. No. 73;
Matches 12; Conservative 5; Mismatches 10; Indels 2; Gaps 2;

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QY      4 KLAHQI-YQFTDKDKDNVAPRSKISPGY 31
Db      138 RLEHDVNIQFPDKDDGN-QPQDQITITGY 165

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RESULT 14
US-09-903-190-174
; Sequence 174, Application US/09903190
; Publication No. US20030162176A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A

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Search completed: October 14, 2003, 08:53:17
Job time : 63 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2003, 08:38:52 ; Search time 405.114 Seconds
(without alignments)
69.629 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main.*
1: /cgn2_6/ptodata/1/paa/pctus_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
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27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
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31: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	163	100.0	31	10	US-08-634-562-9 Sequence 9, Appli

SUMMARIES

2	163	100.0	31	20	US-09-623-548A-938
3	163	100.0	31	20	US-09-657-276-938
4	163	100.0	31	23	US-09-813-345-23
5	163	100.0	31	24	US-09-931-700-3
6	163	100.0	31	24	US-09-931-700-14
7	163	100.0	38	10	US-08-634-562-6
8	163	100.0	40	10	US-08-634-562-11
9	163	100.0	52	1	PCN-US02-22821-2
10	163	100.0	52	20	US-09-623-548A-935
11	163	100.0	52	20	US-09-657-276-935
12	163	100.0	52	23	US-09-813-345-14
13	163	100.0	52	27	US-10-197-954-2
14	163	100.0	52	29	US-10-360-101-7A
15	163	100.0	113	21	US-09-724-676-63615
16	163	100.0	113	21	US-09-724-676A-63615
17	163	100.0	113	32	US-60-453-050-12481
18	163	100.0	113	32	US-60-453-135-12481
19	163	100.0	113	32	US-60-466-412-12481
20	163	100.0	138	32	US-60-453-050-12483
21	163	100.0	138	32	US-60-453-135-12483
22	163	100.0	138	32	US-60-466-412-12483
23	163	100.0	185	8	US-08-484-738A-1
24	163	100.0	185	26	US-10-018-924-2
25	163	100.0	185	26	US-10-030-298-2
26	163	100.0	185	29	US-10-364-889-6
27	163	100.0	185	32	US-60-440-088-148
28	163	100.0	185	32	US-60-453-050-12482
29	163	100.0	185	32	US-60-453-135-12482
30	163	100.0	185	32	US-60-466-412-12482
31	163	100.0	193	28	US-10-206-021-406
32	158	96.9	30	10	US-08-634-562-5
33	157	96.3	188	8	US-08-484-738A-3
34	157	96.3	188	26	US-10-018-924-4
35	157	96.3	188	26	US-10-030-298-4
36	157	96.3	29	10	US-08-634-562-4
37	154	94.5	36	18	US-09-475-158-31
38	150	92.0	36	18	US-09-475-158A-31
39	150	92.0	40	10	US-08-634-562-8
40	150	92.0	50	10	US-08-634-562-7
41	150	92.0	28	10	US-08-634-562-3
42	149	91.4	40	20	US-09-623-548A-944
43	148	90.8	40	20	US-09-657-276-944
44	148	90.8	50	23	US-09-813-345-15

ALIGNMENTS

RESULT 1
US-08-634-562-9
; Sequence 9, Application US/08634562
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Cornish, Jillian
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cooper, Garth J.S.
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS
; NUMBER OF INVENTION: WITH ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/634,562
;; FILING DATE: 18-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Tsao, Y. Rocky
;; REGISTRATION NUMBER: 34,053
;; REFERENCE/DOCKET NUMBER: 08987/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 31 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-634-562-9

Query Match 100.0%; Score 163; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQTDKDKNVAPRSKISPGY 31
Db 1 TVOKLAHQIYQTDKDKNVAPRSKISPGY 31

RESULT 2

US-09-623-548A-938
;; Sequence 938, Application US/09623548A

;; GENERAL INFORMATION:
;; APPLICANT: Conjuchem, Inc.
;; APPLICANT: Bridon, Dominique
;; APPLICANT: Ezrin, Alan
;; APPLICANT: Milner, Peter
;; APPLICANT: Holmes, Darren
;; APPLICANT: Thibaudau, Karen
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;; FILE REFERENCE: 2110

;; CURRENT APPLICATION NUMBER: US/09/623,548A
;; CURRENT FILING DATE: 2000-09-05
;; PRIOR APPLICATION NUMBER: 60/134,406
;; PRIOR FILING DATE: 1999-05-17
;; PRIOR APPLICATION NUMBER: 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-18
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 938
;; LENGTH: 31
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-623-548A-938

Query Match 100.0%; Score 163; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQTDKDKNVAPRSKISPGY 31
Db 1 TVOKLAHQIYQTDKDKNVAPRSKISPGY 31

RESULT 3

US-09-657-276-938
;; Sequence 938, Application US/09657276

;; GENERAL INFORMATION:
;; APPLICANT: Conjuchem, Inc.
;; APPLICANT: Bridon, Dominique
;; APPLICANT: Ezrin, Alan
;; APPLICANT: Milner, Peter
;; APPLICANT: Holmes, Darren
;; APPLICANT: Thibaudau, Karen
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;; FILE REFERENCE: 2110

;; CURRENT APPLICATION NUMBER: US/09/657,276
;; CURRENT FILING DATE: 2000-09-07
;; PRIOR APPLICATION NUMBER: 60/134,406
;; PRIOR FILING DATE: 1999-05-17
;; PRIOR APPLICATION NUMBER: 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-18
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 938
;; LENGTH: 31
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-657-276-938

Query Match 100.0%; Score 163; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQTDKDKNVAPRSKISPGY 31
Db 1 TVOKLAHQIYQTDKDKNVAPRSKISPGY 31

RESULT 4

US-09-813-345-23
;; Sequence 23, Application US/09813345

;; GENERAL INFORMATION:
;; APPLICANT: Smith, Derek D.
;; APPLICANT: Saba, Shankar
;; APPLICANT: Abel, Peter W.

;; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;; SUPERFAMILY AND METHODS OF USE
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Muelling, Raasch & Gebhardt, P.A.
;; STREET: 119 North Fourth Street
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55401

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/813,345
;; FILING DATE: 20-Mar-2001
;; CLASSIFICATION: <Unknown>

;; ATTORNEY/AGENT INFORMATION:
;; NAME: McCormack, Myra H
;; REGISTRATION NUMBER: 36,602
;; REFERENCE/DOCKET NUMBER: 180.00020101
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612/305-1220

TELEFAX: 612/305-1228
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Query Match 100.0%; Score 163; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
 |||||
 Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 5

US-09-931-700-3
 Sequence 3, Application US/09931700
 GENERAL INFORMATION:
 APPLICANT: CUTTITTA, FRANK
 APPLICANT: MARTINEZ, ALFREDO
 APPLICANT: MILLER, MAE JEAN
 APPLICANT: UNSWORTH, EDWARD J.
 APPLICANT: HOOK, WILLIAM
 APPLICANT: WALSH, THOMAS
 APPLICANT: GREY, KAREN
 APPLICANT: MACRI, CHARLES
 TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
 TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
 TITLE OF INVENTION: Physiology
 FILE REFERENCE: 2026-4202US4
 CURRENT APPLICATION NUMBER: US/09/931,700
 CURRENT FILING DATE: 2001-08-16
 PRIOR APPLICATION NUMBER: 09/011,922
 PRIOR FILING DATE: 1998-02-17
 PRIOR APPLICATION NUMBER: PCT/US96/13286
 PRIOR FILING DATE: 1996-08-16
 PRIOR APPLICATION NUMBER: US/60/013,172
 PRIOR FILING DATE: 1996-03-12
 PRIOR APPLICATION NUMBER: US60/002,936
 PRIOR FILING DATE: 1995-08-30
 PRIOR APPLICATION NUMBER: US/60/002,514
 PRIOR FILING DATE: 1995-08-18
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Peptide, P072,
 OTHER INFORMATION: PreproAM (amino acids 116-146)

Query Match 100.0%; Score 163; DB 24; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
 |||||
 Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 6

US-09-931-700-14
 Sequence 14, Application US/09931700
 GENERAL INFORMATION:
 APPLICANT: CUTTITTA, FRANK

APPLICANT: MARTINEZ, ALFREDO
 APPLICANT: MILLER, MAE JEAN
 APPLICANT: UNSWORTH, EDWARD J.
 APPLICANT: HOOK, WILLIAM
 APPLICANT: WALSH, THOMAS
 APPLICANT: GREY, KAREN
 APPLICANT: MACRI, CHARLES
 TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
 TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
 TITLE OF INVENTION: Physiology
 FILE REFERENCE: 2026-4202US4
 CURRENT APPLICATION NUMBER: US/09/931,700
 CURRENT FILING DATE: 2001-08-16
 PRIOR APPLICATION NUMBER: 09/011,922
 PRIOR FILING DATE: 1998-02-17
 PRIOR APPLICATION NUMBER: PCT/US96/13286
 PRIOR FILING DATE: 1996-08-16
 PRIOR APPLICATION NUMBER: US/60/013,172
 PRIOR FILING DATE: 1996-03-12
 PRIOR APPLICATION NUMBER: US60/002,936
 PRIOR FILING DATE: 1995-08-30
 PRIOR APPLICATION NUMBER: US/60/002,514
 PRIOR FILING DATE: 1995-08-18
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 14
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Peptide,
 OTHER INFORMATION: Synthetic homology of AM (P072), Structural amino
 OTHER INFORMATION: acid sequence representing two-thirds of the
 OTHER INFORMATION: intact AM peptide
 US-09-931-700-14

Query Match 100.0%; Score 163; DB 24; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
 |||||
 Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 7

US-08-634-562-6
 Sequence 6, Application US/08634562
 GENERAL INFORMATION:
 APPLICANT: COY, David H.
 APPLICANT: Cornish, Jillian
 APPLICANT: Reid, Ian Reginald
 APPLICANT: Cooper, Garth J.S.
 TITLE OF INVENTION: TREATMENT OF BONE DISORDERS
 TITLE OF INVENTION: WITH ADRENOMEDULLIN
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/634,562
 FILING DATE: 18-APR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

```
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 08987/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-634-562-6

Query Match      100.0%; Score 163; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
    |||||
Db 8 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 38

RESULT 8
US-08-634-562-11
; Sequence 11, Application US/08634562
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Cornish, Jillian
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cooper, Garth J.S.
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS
; TITLE OF INVENTION: WITH ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,562
; FILING DATE: 18-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 08987/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-634-562-11

Query Match      100.0%; Score 163; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 08987/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-634-562-6

Query Match      100.0%; Score 163; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
    |||||
Db 8 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 38

RESULT 9
PCT-US02-22821-2
; Sequence 2, Application PC/TUS0222821
; GENERAL INFORMATION:
; APPLICANT: HK Pharmaceuticals, Inc.
; APPLICANT: Kolster, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: PCT/US02/22821
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo Sapien
; PCT-US02-22821-2

Query Match      100.0%; Score 163; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
    |||||
Db 22 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 52

RESULT 10
US-09-623-548A-935
; Sequence 935, Application US/09623548A
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibodeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 935
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-935

Query Match 100.0%; Score 163; DB 20; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 22 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 52

RESULT 11

US-09-657-276-935
; Sequence 935, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 935
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-935

Query Match 100.0%; Score 163; DB 20; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 22 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 52

RESULT 12

US-09-813-345-14
; Sequence 14, Application US/09813345
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; Saha, Shankar
; Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Muelling, Raasch & Gebhardt, P.A.
; STREET: 119 North Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,345
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-813-345-14

Query Match 100.0%; Score 163; DB 23; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 22 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 52

RESULT 13

US-10-197-954-2
; Sequence 2, Application US/10197954
; GENERAL INFORMATION:
; APPLICANT: K*ster, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 52
; ORGANISM: Homo Sapien
US-10-197-954-2

Query Match 100.0%; Score 163; DB 27; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 22 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 52

RESULT 14

US-10-360-101-74
; Sequence 74, Application US/10360101


```
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A13,S16-sequence of Adrenomedullin Hypotensive peptide
US-10-360-101-74
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Query Match      100.0%; Score 163; DB 29; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
      |||||||||||||||||||||||||||||||
Db      22 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 52
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RESULT 15
US-09-724-676-63615
; Sequence 63615, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63615
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-63615
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Query Match      100.0%; Score 163; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
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Db      44 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 74
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Search completed: October 14, 2003, 08:51:05
Job time : 406.114 secs